

GenCore version 5.1.6
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OM protein - protein search, using sw model.

Run on: February 25, 2005, 02:05:51 ; Search time 165 Seconds
(without alignments)
866.033 Million cell updates/sec

Title: US-10-749-990-2

Perfect score: 1922
Sequence: 1 MDLCKPKMSVLVALVIFQ.....RHRRSSMSVEAETTTTSP 378

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_16Dec04:*

1: Geneseqp1980s:*\n2: Geneseqp1990s:*\n3: Geneseqp2000s:*\n4: Geneseqp2001s:*\n5: Geneseqp2002s:*\n6: Geneseqp2003as:*\n7: Geneseqp2003bs:*\n8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	1922	100.0	378	2	AA54079 Epstein B
2	1922	100.0	378	2	AA53622 Epstein B
3	1922	100.0	378	2	AA56164 G-protein
4	1922	100.0	378	8	ADR03499 Cytokine
5	1907	99.2	378	2	AAW48724 Human VAI
6	1907	99.2	378	2	AAW48724 Human VAI
7	1907	99.2	378	4	AAW48724 Human VAI
8	1907	99.2	378	4	AAW48724 Human VAI
9	1907	99.2	378	5	AAW48724 Human VAI
10	1907	99.2	378	6	AAW48724 Human VAI
11	1907	99.2	378	6	AAW48724 Human VAI
12	1907	99.2	378	7	AAW48724 Human VAI
13	1907	99.2	378	7	AAW48724 Human VAI
14	1907	99.2	378	8	AAW48724 Human VAI
15	1907	99.2	378	8	AAW48724 Human VAI
16	1907	99.2	378	8	AAW48724 Human VAI
17	1907	99.2	378	8	AAW48724 Human VAI
18	1907	99.2	378	8	AAW48724 Human VAI
19	1907	99.2	378	8	AAW48724 Human VAI
20	1907	99.2	378	8	AAW48724 Human VAI
21	1904	99.1	378	8	AAW48724 Human VAI
22	1903	99.0	378	8	AAW48724 Human VAI
23	1901	98.9	378	3	AAW48724 Human VAI
24	1900	98.9	378	3	AAW48724 Human VAI
25	1900	98.9	378	7	AAW48724 Human VAI

26	1900	98.9	378	7	ADH14196	Adh14196 Mutated h
27	1892	98.4	569	4	ABG12373	Abg12373 Novel hum
28	1814	94.4	410	2	AAW53743	AAW53743 Putative
29	1814	94.4	410	2	AAW48723	AAW48723 Polyptepi
30	1814	94.4	410	2	AAW21687	AAW21687 Genomic c
31	1814	94.4	410	5	AAU91229	AAU91229 Human 7 c
32	1813	94.3	358	2	AAW53745	AAW53745 Partial b
33	1813	94.3	358	2	AAW21689	AAW21689 Human 7TM
34	1813	94.3	358	5	AAU91231	AAU91231 Human 7 c
35	1795.5	93.4	361	2	AAW97348	AAW97348 An Epstei
36	1787	93.0	496	6	ABG76343	Abg76343 Mouse rec
37	1787	93.0	578	6	ABG76344	Abg76344 Mouse rec
38	1701	88.5	404	8	ADR66957	ADR66957 Mouse can
39	1696	88.2	378	5	AAW21699	AAW21699 7TM recep
40	1696	88.2	378	5	AAU91241	AAU91241 Mouse 7 c
41	1696	88.2	378	8	ADO29232	ADO29232 Mouse GPC
42	1602.5	83.4	359	2	AAW53747	AAW53747 Seven tra
43	1602.5	83.4	359	2	AAW48728	AAW48728 Murine V3
44	1602.5	83.4	359	3	AAW21691	AAW21691 Murine 7T
45	1602.5	83.4	359	5	AAU91233	AAU91233 Mouse 7 c

ALIGNMENTS

AA54079	standard; protein; 378 AA.
ADH14196	Adh14196 Mutated h
ABG12373	Abg12373 Novel hum
AAW53743	AAW53743 Putative
AAW48723	AAW48723 Polyptepi
AAW21687	AAW21687 Genomic c
AAU91229	AAU91229 Human 7 c
AAW53745	AAW53745 Partial b
AAW21689	AAW21689 Human 7TM
AAU91231	AAU91231 Human 7 c
AAW97348	AAW97348 An Epstei
ABG76343	Abg76343 Mouse rec
ABG76344	Abg76344 Mouse rec
ADR66957	ADR66957 Mouse can
AAW21699	AAW21699 7TM recep
AAU91241	AAU91241 Mouse 7 c
ADO29232	ADO29232 Mouse GPC
AAW53747	AAW53747 Seven tra
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ABG12373	Abg12373 Novel hum
AAW53743	AAW53743 Putative
AAW48723	AAW48723 Polyptepi
AAW21687	AAW216

PF 08-OCT-1993; 93WO-US009636.
XX
PR 25-NOV-1992; 92US-00980518.
XX
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
XX
PI Birkenbach M, Kieff E;
XX
XX WPI; 1994-200183/24.
DR N-PSDB; AAQ64125.
XX
PT DNA coding for Epstein Barr Virus induced (EBI) polypeptide(s) and
PT antibodies to EBV1, 2 and 3 - useful for detecting EBV by hybridisation
PT or by immunosassay.
XX
PS Claim 8; Page 54-56; 84pp; English.
XX
CC EBV infected B lymphocytes recapitulate features of antigen stimulation
CC in enlarging, increasing RNA synthesis, expressing activation antigens
CC and adhesion molecules, secreting Ig and proliferating. Unlike antigen
CC stimulated B lymphocytes, EBV infected B lymphocytes continue to
CC proliferate (in vitro) as immortalised lymphoblastoid cell lines. Because
CC of the similar effects of EBV and antigen, EBV induced genes are likely
CC to include mediators of antigen induced B lymphocyte growth or
CC differentiation. (Updated on 25-MAR-2003 to correct PM field.)
XX
SQ Sequence 378 AA;

Query Match 100.0%; Score 1922; DB 2; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.9e-206;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLGPMSKSVLVVALLVIFQVCLCODEVTDDYIGDNTTVDYTLFESLCSKQDVNPKAF 60
DB 1 MDLGPMSKSVLVVALLVIFQVCLCODEVTDDYIGDNTTVDYTLFESLCSKQDVNPKAF 60
QY 61 LPIWYSIIICFVGLGNGLVLTYYIFPKRLKMTDTYLLNLAVADILFLTLTPMAYSAAK 120
DB 61 LPIWYSIIICFVGLGNGLVLTYYIFPKRLKMTDTYLLNLAVADILFLTLTPMAYSAAK 120
QY 121 SWEGVHFCKLIPIAYKMSFFSGMLLLCISIDRYVAIVQAVSAHRHARVLLISKSCV 180
DB 121 SWEGVHFCKLIPIAYKMSFFSGMLLLCISIDRYVAIVQAVSAHRHARVLLISKSCV 180
QY 121 SWEGVHFCKLIPIAYKMSFFSGMLLLCISIDRYVAIVQAVSAHRHARVLLISKSCV 180
DB 121 SWEGVHFCKLIPIAYKMSFFSGMLLLCISIDRYVAIVQAVSAHRHARVLLISKSCV 180
QY 181 GSALIAVLSIPBLLYSDDLQSSSEQAMRCSLITEHVEAFITIOVAQVAVIGFLVPLAMS 240
DB 181 GSALIAVLSIPBLLYSDDLQSSSEQAMRCSLITEHVEAFITIOVAQVAVIGFLVPLAMS 240
QY 241 FCYVITIRTLQARNFERNKAIKVIIAVVVFIYFQLPYNGVLAQVTANFNITSSCEL 300
DB 241 FCYVITIRTLQARNFERNKAIKVIIAVVVFIYFQLPYNGVLAQVTANFNITSSCEL 300
QY 301 SKQINIAVDVYSLACVRCVNPFLYAFIGVFRNDIFKLFKDLGCLSOBOLRQWSSCRH 360
DB 301 SKQINIAVDVYSLACVRCVNPFLYAFIGVFRNDIFKLFKDLGCLSOBOLRQWSSCRH 360
QY 361 IRRSSMSVEAETTTTFFSP 378
DB 361 IRRSSMSVEAETTTTFFSP 378

RESULT 2
AAWS3622
ID AAWS3622 standard; protein; 378 AA.
XX
AC AAWS3622;

DT 09-JUL-1998 (first entry)
XX
DE Epstein Barr virus induced protein 1 (EBI-1).
XX
KM Assessing; monitoring; foetal development; placental development;
KM Epstein Barr virus; EBV; induced gene 1; EBI-1.

XX Homo sapiens.
OS
XX
XX US5744301-A.
XX
XX 28-APR-1998.
PD
XX
PF 02-FEB-1995; 95US-00383750.
XX
XX
PR 25-NOV-1992; 92US-00980518.
PR 30-NOV-1994; 94US-00352678.
XX
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
XX
XX Kieff E, Birkenbach M;
PI
XX WPI; 1998-271060/24.
DR N-PSDB; AAV25490.
XX
PT Assessing or monitoring foetal or placental development - comprises
PT detecting the level or size of Epstein Barr virus induced nucleic acid or
PT protein in maternal serum samples.
XX
PS Example 2; Col 37-40; 45pp; English.
XX
CC The present sequence was used in the development of a novel method for
CC assessing or monitoring foetal or placental development. The method
CC comprises taking a maternal serum sample, and detecting the level or size
CC of Epstein Barr virus (EBV) induced gene or protein 3 (EBI-3) to obtain a
CC result, which can be compared to a control to assess or monitor foetal or
CC placental development
XX
SQ Sequence 378 AA;

Query Match 100.0%; Score 1922; DB 2; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.9e-206;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLGPMSKSVLVVALLVIFQVCLCODEVTDDYIGDNTTVDYTLFESLCSKQDVNPKAF 60
DB 1 MDLGPMSKSVLVVALLVIFQVCLCODEVTDDYIGDNTTVDYTLFESLCSKQDVNPKAF 60
QY 61 LPIWYSIIICFVGLGNGLVLTYYIFPKRLKMTDTYLLNLAVADILFLTLTPMAYSAAK 120
DB 61 LPIWYSIIICFVGLGNGLVLTYYIFPKRLKMTDTYLLNLAVADILFLTLTPMAYSAAK 120
QY 121 SWEGVHFCKLIPIAYKMSFFSGMLLLCISIDRYVAIVQAVSAHRHARVLLISKSCV 180
DB 121 SWEGVHFCKLIPIAYKMSFFSGMLLLCISIDRYVAIVQAVSAHRHARVLLISKSCV 180
QY 121 SWEGVHFCKLIPIAYKMSFFSGMLLLCISIDRYVAIVQAVSAHRHARVLLISKSCV 180
DB 121 SWEGVHFCKLIPIAYKMSFFSGMLLLCISIDRYVAIVQAVSAHRHARVLLISKSCV 180
QY 181 GSALIAVLSIPBLLYSDDLQSSSEQAMRCSLITEHVEAFITIOVAQVAVIGFLVPLAMS 240
DB 181 GSALIAVLSIPBLLYSDDLQSSSEQAMRCSLITEHVEAFITIOVAQVAVIGFLVPLAMS 240
QY 241 FCYVITIRTLQARNFERNKAIKVIIAVVVFIYFQLPYNGVLAQVTANFNITSSCEL 300
DB 241 FCYVITIRTLQARNFERNKAIKVIIAVVVFIYFQLPYNGVLAQVTANFNITSSCEL 300
QY 301 SKQINIAVDVYSLACVRCVNPFLYAFIGVFRNDIFKLFKDLGCLSOBOLRQWSSCRH 360
DB 301 SKQINIAVDVYSLACVRCVNPFLYAFIGVFRNDIFKLFKDLGCLSOBOLRQWSSCRH 360
QY 361 IRRSSMSVEAETTTTFFSP 378
DB 361 IRRSSMSVEAETTTTFFSP 378

RESULT 3
AAWS6164
ID AAWS6164 standard; protein; 378 AA.
XX
AC AAWS6164;

XX

DT 20-JUL-1998 (first entry)
 XX G-protein coupled receptor (R7G) designated EB11.
 XX Lymphocyte R7G; EB11; G-protein coupled receptor;
 XX opiate/opioid recognition site; opiate; opioid; opioid binding protein;
 KW screening; lymphocyte receptor; compound; agonist; antagonist;
 KW lymphocyte receptor protein; immune-cell specific lymphocyte receptor;
 KW neuronal type opioid receptor.
 XX Homo sapiens.
 OS
 XX US5753516-A.
 PN 19-MAY-1998.
 PD 03-FEB-1995; 95US-00383751.
 XX 03-FEB-1995; 95US-00383751.
 PR 03-FEB-1995; 95US-00383751.
 XX (FINB/) FINBERG R W.
 PA (HEAG/) HEAGY W E.
 XX Heagy WE, Finberg RW;
 PI WPI; 1998-311410/27.
 DR N-PSDB; AAV22684.
 XX Screening assay for lymphocyte opioid receptor ligands - using
 PT recombinant receptor protein.
 PT Claim 1; Col 87-88; 70pp; English.
 XX
 PS The present sequence represents a novel lymphocyte R7G, termed EB11. R7G
 CC proteins are part of the G-protein coupled receptor superfamily. EB11 is
 CC a functional opiate/opioid recognition site that probably plays a major
 CC role in mediating the effects that opiate/opioids have on lymphocytes.
 CC The EB11 protein is an opioid binding protein that is displayed on the
 CC surface of lymphocytes. A process for screening a candidate substance for
 CC ability to interact with a lymphocyte receptor comprises selecting a
 CC candidate substance having a chemical structure or biological activity
 CC suggestive of an ability to mimic the biological activity of an opiate,
 CC opioid drug or opioid peptide having known binding affinity for EB11. The
 CC ability of the candidate substance is tested to interact with the
 CC lymphocyte receptor protein. This method can be used to screen for
 CC agonists or antagonists to the lymphocyte receptor protein. The method
 CC can be modified and used to screen for agonists or antagonists to the
 CC immune-cell specific lymphocyte receptor polypeptide or the neuronal type
 CC opioid receptor polypeptide
 CC
 XX Sequence 378 AA;
 SQ
 Query Match 100.0%; Score 1922; DB 2; Length 378;
 Best Local Similarity 100.0%; Pred. No. 1.9e-206;
 Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 MDLGRKMSVLLVALLVIFQVCLCODBYTDDYIGDNTYDTYLFESLCKKQVRNFKAMF 60
 1 MDLGRKMSVLLVALLVIFQVCLCODBYTDDYIGDNTYDTYLFESLCKKQVRNFKAMF 60
 61 LPIWYIIICFVGLGNGVLVLYYFKRLKMTDTYLLMLAVADILFLLTLPWYSAK 120
 61 LPIWYIIICFVGLGNGVLVLYYFKRLKMTDTYLLMLAVADILFLLTLPWYSAK 120
 121 SWVFGVHFKLFAIYKMSFSGMILLTISIDRYVAIVQVSAHRRARVLLISLSCV 180
 121 SWVFGVHFKLFAIYKMSFSGMILLTISIDRYVAIVQVSAHRRARVLLISLSCV 180
 181 GSAILATVSIPELAYSDELORSSSEQAMRCSLITEHVAFTITQVQMTYIGFLVPLAMS 240
 181 GSAILATVSIPELAYSDELORSSSEQAMRCSLITEHVAFTITQVQMTYIGFLVPLAMS 240
 241 FCYLVIRTLQARNERNKAIVIIAVVVFIVFLQPYNGVVLQAVANFNITSSTCEL 300

DB 241 FCYLVIRTLQARNERNKAIVIIAVVVFIVFLQPYNGVVLQAVANFNITSSTCEL 300
 QY 301 SKQNLNADVTYSLACVRCVNPFLVAFIGVFRNDIFPLFDLGLSLQSLQSSCRH 360
 DB 301 SKQNLNADVTYSLACVRCVNPFLVAFIGVFRNDIFPLFDLGLSLQSLQSSCRH 360
 QY 361 IRRSSMSVEAFTTTTSP 378
 DB 361 IRRSSMSVEAFTTTTSP 378
 RESULT 4
 ADR03499
 ID ADR03499 standard; protein; 378 AA.
 XX
 AC ADR03499;
 XX
 DT 21-OCT-2004 (first entry)
 XX
 DE Cytokine receptor CCR7.
 XX
 KW antiallergic; antiinflammatory; antimicrobial; cytostatic;
 KW immunostimulant; immunosuppressive; CCX chemokine receptor; CCX CKR;
 KW EB11-13 and chemokine; ELC; secondary lymphoid-tissue chemokine; SLC;
 KW thymus-expressed chemokine; TECK; chemokine binding activity;
 KW CCX CKR modulator; chemokine binding modulator; inflammation; allergy;
 KW autoimmune disease; graft rejection; cancer; infectious disease;
 KW immunosuppressive disease; CCR7.
 XX
 OS Unidentified.
 XX
 PN US2004146926-A1.
 XX
 PD 29-JUL-2004.
 XX
 PF 24-FEB-2004; 2004US-00787018.
 XX
 PR 12-OCT-1999; 99US-0159015P.
 PR 13-OCT-1999; 99US-0159210P.
 PR 20-DEC-1999; 99US-0172979P.
 PR 28-DEC-1999; 99US-0173388P.
 PR 03-MAR-2000; 2000US-0186626P.
 PR 10-OCT-2000; 2000US-00686019.
 PR 21-NOV-2000; 2000US-00721495.
 XX
 PA (CHEM-) CHEMOCENTRXX INC.
 XX
 PI Gosling J, Dairaghi DJ, Hanley M, Miao Z, Talbot D, Schall TJ;
 DR WPI; 2004-561394/54.
 XX
 PT New CCX chemokine receptor polypeptide that binds ELC, SLC or TECK,
 PT useful in identifying modulators of its expression or activity which are
 PT potentially useful for treating inflammation, allergies, autoimmune
 PT disease and cancer.
 XX
 PS Example 1; Fig 2a; 37pp; English.
 XX
 CC The invention describes an isolated or recombinant CCX chemokine receptor
 CC (CCX CKR) polypeptide (1) or its fragment that binds EB11-13 and
 CC chemokine (ELC), secondary lymphoid-tissue chemokine (SLC) or thymus-
 CC expressed chemokine (TECK). Also described are: a fusion protein
 CC comprising the polypeptide; an isolated polynucleotide encoding (1) or
 CC its fragment; an isolated polynucleotide comprising a sequence encoding a
 CC polypeptide that has a chemokine binding activity which is: a
 CC polynucleotide comprising the sequence of SEQ ID NO:1 or SEQ ID NO:3; a
 CC polynucleotide that hybridises under stringent conditions to (a); or a
 CC polynucleotide sequence which is degenerate as a result of the genetic
 CC code to the sequences defined in (a) or (b); a recombinant (expression)
 CC vector comprising the polynucleotide; a host cell comprising the vector;
 CC producing a CCX CKR protein, peptide or fusion protein; a polynucleotide
 CC primer, probe, antisense oligonucleotide or ribozyme comprising at least

15 contiguous bases identical or exactly complementary to the 1147-bp sequence; an antibody or its fragment that specifically binds to the polypeptide; an isolated cell capable of secreting the antibody; a hybridoma capable of secreting the antibody; detecting a CCX CKR gene product in a sample; amplifying a CCX CKR polynucleotide in a sample; identifying a modulator of the binding of CCX CKR to a chemokine; producing a pharmaceutical composition from a modulator of CCX CKR (chemokine binding) activity; identifying a modulator of CCX CKR activity; and treating a CCX CKR-mediated condition in a mammal. Agents that modulate the activity of CCX CKR in a cell or tissue in an animal are useful for treating CCX CKR related conditions such as inflammation, allergy, an autoimmune disease, graft rejection, cancer, an infectious disease or an immunosuppressive disease, preferably inflammation. This is the amino acid sequence of a cytokine receptor CCR7, used in a comparison with human cytokine receptor CCX CKR of the invention.

Sequence 378 AA;

Query Match 100.0%; Score 1922; DB 8; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.9e-206;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLGRPKSVLVVALLVIFQVCLCODEVTDDYIGNTTVDTYLPESLCSKKDVRNFKAMF 60
DB 1 MDLGRPKSVLVVALLVIFQVCLCODEVTDDYIGNTTVDTYLPESLCSKKDVRNFKAMF 60
QY 61 LPIMYSIICFVGLGNGLVLTYYIFKRLKTMTDYTLNLAVADILFLTLPPMAYSAAK 120
DB 61 LPIMYSIICFVGLGNGLVLTYYIFKRLKTMTDYTLNLAVADILFLTLPPMAYSAAK 120
QY 121 SWFGVHFCKLIIFAIYKMSFSGMILLICISIDRYVAIVQAVSAHRHRAVLLISKSCV 180
DB 121 SWFGVHFCKLIIFAIYKMSFSGMILLICISIDRYVAIVQAVSAHRHRAVLLISKSCV 180
QY 181 GSALIAATVLSIPELLYSLORSSSEQAMRCSLITEHVAFTTIOVAQWVIGFVPLLAMS 240
DB 181 GSALIAATVLSIPELLYSLORSSSEQAMRCSLITEHVAFTTIOVAQWVIGFVPLLAMS 240
QY 241 FCYLVITRTLLQARNFERNKAIKVIAVAVVFIVQLPYNGVLAQTVANFNITSSTCEL 300
DB 241 FCYLVITRTLLQARNFERNKAIKVIAVAVVFIVQLPYNGVLAQTVANFNITSSTCEL 300
QY 301 SKQINIAVDVTSIACVRCVNPFLYAFIGVFRNDIFKLPFDLGCLSOEQLRQWSSCRH 360
DB 301 SKQINIAVDVTSIACVRCVNPFLYAFIGVFRNDIFKLPFDLGCLSOEQLRQWSSCRH 360
QY 361 IRRSSMSVEAETTTTFSP 378
DB 361 IRRSSMSVEAETTTTFSP 378

RESULT 5
AAW48724
ID AAW48724 standard; protein; 378 AA.

AAW48724;

DT 25-SEP-1998 (first entry)

DE Human V31 seven transmembrane receptor.

KW V28; placenta; seven transmembrane receptor; 7TM; signal transduction;

KM immunology; inflammation; V31.

XX Homo sapiens.

FT Key Location/Qualifiers

FT Domain 58..86

FT Domain /note= "Transmembrane domain 1"

FT Domain 96..119

FT Domain /note= "Transmembrane domain 2"

FT Domain 131..152

FT Domain /note= "Transmembrane domain 3"

FT Domain 171..196
FT /note= "Transmembrane domain 4"
FT Domain 219..247
FT /note= "Transmembrane domain 5"
FT Domain 264..285
FT /note= "Transmembrane domain 6"
FT Domain 306..331
FT /note= "Transmembrane domain 7"

US5759804-A.

02-JUN-1998.

17-NOV-1993; 93US-00153848.

17-NOV-1992; 92US-00977452.

(ICOS-) ICOS CORP.

Schweickart VL, Godiska R, Gray PW;

WPI, 1998-332132/29.

N-PESDB; AAV18347.

DNA encoding V28 seven transmembrane receptor polypeptide - useful for producing recombinant polypeptide and anti-V28 antibodies, and in screening assays for V28 agonists and antagonists.

Example 3; Col 39-42; 56pp; English.

The present sequence represents the V31 seven transmembrane (7TM) receptor encoded by the V31 cDNA (AAV18347). The invention claims for a full length V28 genomic DNA (AAV18343) and the V28 protein it encodes (AAW48722). V28 and V31 proteins are 7TM receptors which are probably involved in signal transduction. The invention also claims that cells transformed with V28 DNA can be used to produce the recombinant polypeptide, to produce anti-V28 antibodies or in screening assays for V28 agonists or antagonists. The antibodies, agonists and antagonists could then be used to modulate V28 receptor-ligand binding, for e.g. in immunological and/or inflammatory events in vivo

Sequence 378 AA;

Query Match 99.2%; Score 1907; DB 2; Length 378;
Best Local Similarity 99.2%; Pred. No. 9.1e-205;
Matches 375; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDLGRPKSVLVVALLVIFQVCLCODEVTDDYIGNTTVDTYLPESLCSKKDVRNFKAMF 60
DB 1 MDLGRPKSVLVVALLVIFQVCLCODEVTDDYIGNTTVDTYLPESLCSKKDVRNFKAMF 60
QY 61 LPIMYSIICFVGLGNGLVLTYYIFKRLKTMTDYTLNLAVADILFLTLPPMAYSAAK 120
DB 61 LPIMYSIICFVGLGNGLVLTYYIFKRLKTMTDYTLNLAVADILFLTLPPMAYSAAK 120
QY 121 SWFGVHFCKLIIFAIYKMSFSGMILLICISIDRYVAIVQAVSAHRHRAVLLISKSCV 180
DB 121 SWFGVHFCKLIIFAIYKMSFSGMILLICISIDRYVAIVQAVSAHRHRAVLLISKSCV 180
QY 181 GSALIAATVLSIPELLYSLORSSSEQAMRCSLITEHVAFTTIOVAQWVIGFVPLLAMS 240
DB 181 GSALIAATVLSIPELLYSLORSSSEQAMRCSLITEHVAFTTIOVAQWVIGFVPLLAMS 240
QY 241 FCYLVITRTLLQARNFERNKAIKVIAVAVVFIVQLPYNGVLAQTVANFNITSSTCEL 300
DB 241 FCYLVITRTLLQARNFERNKAIKVIAVAVVFIVQLPYNGVLAQTVANFNITSSTCEL 300
QY 301 SKQINIAVDVTSIACVRCVNPFLYAFIGVFRNDIFKLPFDLGCLSOEQLRQWSSCRH 360
DB 301 SKQINIAVDVTSIACVRCVNPFLYAFIGVFRNDIFKLPFDLGCLSOEQLRQWSSCRH 360
QY 361 IRRSSMSVEAETTTTFSP 378
DB 361 IRRSSMSVEAETTTTFSP 378

DB 361 IRRSSMSVEAETTTTSP 378

RESULT 6
AAB21688
ID AAB21688 standard; protein; 378 AA.
XX
AC AAB21688;
XX
DT 26-JAN-2001 (first entry)
XX
DE Human 7TM receptor V31-B cDNA clone protein.
XX
KW Seven transmembrane receptor; 7TM; heptahelical; serpentine;
KM G-protein-coupled; V28; V31; V112; R20; R2; R12; RM3; gene therapy;
XX cancer.
XX
OS Homo sapiens.
XX
PN US6107475-A.
XX
PD 22-AUG-2000.
XX
PF 26-APR-1999; 99US-00299843.
XX
PR 17-NOV-1992; 92US-00977452.
PR 17-NOV-1993; 93US-00153848.
PR 17-MAY-1994; 94US-00245242.
PR 01-JUN-1998; 98US-00088337.
XX
PA (ICOS-) ICOS CORP.
XX
PI Schwellkart VL, Gray PW, Godiska R;
XX
DR WPI, 2000-571335/53.
DR N-PSDB; AAA91707.
XX
XX Polynucleotide encoding seven transmembrane receptors, antibody specific
PT to the receptor, agonist and antagonist of the receptor useful for
PT treating inflammation in a mammal.
XX
PS Example 3; Col 41-44; 61pp; English.
XX
CC The present sequence is a novel seven transmembrane (7TM) receptors (also
CC known as heptahelical, serpentine or G-protein-coupled receptors). The
CC coding sequence for the present sequence may be used for gene therapy for
CC diseases such as cancer
XX
SQ Sequence 378 AA;

Query Match 99.2%; Score 1907; DB 3; Length 378;
Best Local Similarity 99.2%; Pred. No. 9.1e-205;
Matches 375; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDLGRKMSVLLVALLVIFQVCLCODEVTDDYIGDNTTVDYTLFBSLCSKRDVRNFKAMF 60
DB 1 MDLGRKMSVLLVALLVIFQVCLCODEVTDDYIGDNTTVDYTLFBSLCSKRDVRNFKAMF 60
QY 61 LPIWMSIIFPVGLGNGLVLLTYIYRKLKMTDTYLLANVADILFLTLPPWASAAK 120
DB 61 LPIWMSIIFPVGLGNGLVLLTYIYRKLKMTDTYLLANVADILFLTLPPWASAAK 120
QY 121 SWVFGVHFCKLFAIYKMSFPGMLLLCISIDRYVAIVQAVSAHRHRAVLLISLSCV 180
DB 121 SWVFGVHFCKLFAIYKMSFPGMLLLCISIDRYVAIVQAVSAHRHRAVLLISLSCV 180
QY 181 GSAILATVLSIDELYSIDLRSSSEQAMRCSLITEHVEAFITIQVAMVIGFLVPLLAAS 240
DB 181 GSAILATVLSIDELYSIDLRSSSEQAMRCSLITEHVEAFITIQVAMVIGFLVPLLAAS 240
QY 241 FCYLVIRTLQARNERNKAIVYIAVVVFVFPOLPNGVTLAOTVANFNITSTCEI 300
DB 241 FCYLVIRTLQARNERNKAIVYIAVVVFVFPOLPNGVTLAOTVANFNITSTCEI 300

QY 301 SKQNLINADVTVSLACVRCVNPFLYAFIGVFRNDIFLFDLGLSGLSGLRQSSGCH 360
DB 301 SKQNLINADVTVSLACVRCVNPFLYAFIGVFRNDIFLFDLGLSGLSGLRQSSGCH 360
QY 361 IRRSSMSVEAETTTTSP 378
DB 361 IRRSSMSVEAETTTTSP 378

RESULT 7
AAG80114
ID AAG80114 standard; protein; 378 AA.
XX
AC AAG80114;
XX
DT 17-JAN-2002 (first entry)
XX
DE Human CCR7 protein.
XX
KW Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;
KM inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;
KM chronic bowel inflammation; rheumatoid arthritis; cytostatic;
KM antineoplastic; antineoplastic; immunosuppressive; dermatological;
XX antineoplastic; antineoplastic.
XX
OS Homo sapiens.
XX
PN WO200172830-A2.
XX
PD 04-OCT-2001.
XX
PF 02-APR-2001; 2001WO-EP003708.
XX
PR 31-MAR-2000; 2000DE-01016013.
XX
PA (IPFP-) IFF PHARM GMBH.
PA (FORS/) FORSMANN U.
XX
PI Forsemann W, Adermann K, Heiland A, Spodeberg N;
XX
DR WPI, 2001-626256/72.
XX
PT Diagnostic agent containing two or more receptor-specific ligands, useful
PT for detecting tumors, inflammation etc., also therapeutic use of ligand
PT inhibitors.
XX
PS Disclosure; Page 10; 26pp; German.
XX
CC This invention describes a novel diagnostic agent (A) comprising at least
CC two different ligands (I) for receptors (II) that are implicated in
CC disease. (A) are used for the diagnosis of tumors (especially colorectal
CC or prostatic), organ rejection, inflammation and autoimmune diseases.
CC Also inhibitors of (I) are used therapeutically against tumors (and their
CC metastases), inflammation (particularly bronchial asthma or chronic bowel
CC inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),
CC where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,
CC endocrine, motor or urogenital systems or skin are affected, and bone
CC marrow diseases. The products of the invention are chemokine derivatives
CC which have cytostatic, antiinflammatory, antineoplastic,
CC immunosuppressive, dermatological, antineoplastic, antineoplastic.
CC Chemokines act on specific tumor and inflammatory cells through a
CC constellation of chemokine receptors (CR), which control migration and
CC proliferation of these cells. AAG80045-AAG80128 represent human chemokine
CC fragments used to illustrate the method of the invention
XX
SQ Sequence 378 AA;

Query Match 99.2%; Score 1907; DB 4; Length 378;
Best Local Similarity 99.2%; Pred. No. 9.1e-205;
Matches 375; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDLGRKMSVLLVALLVIFQVCLCODEVTDDYIGDNTTVDYTLFBSLCSKRDVRNFKAMF 60

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Db      1 MDLGRKMSVLLVALLVIFQVCLCODEVTDYIGDNTVDYTLFSLCSKKQVRNFKAMF 60
Qy      61 LPIMYSIICFVGLGNGLVVLTYYIFKRLKTMTDYTLNLAVADILFLTLPEFMAVSAK 120
Db      61 LPIMYSIICFVGLGNGLVVLTYYIFKRLKTMTDYTLNLAVADILFLTLPEFMAVSAK 120
Qy      121 SWFGVHFCKLIFAIYKMSFSGMILLICISIDRYVAIVQAVSAHRHARVLLISKSCV 180
Db      121 SWFGVHFCKLIFAIYKMSFSGMILLICISIDRYVAIVQAVSAHRHARVLLISKSCV 180
Qy      181 GSAILATVLSIPELLYSDLRSSSEQAMRCSLITEHVEAFITIQVAVWIGFVPLLAMS 240
Db      181 GIMILATVLSIPELLYSDLRSSSEQAMRCSLITEHVEAFITIQVAVWIGFVPLLAMS 240
Qy      241 FCYLVITIRTLQARNPERKAIKVIIVAVVFIIVQLPYNGVLAQTVAENFITSSTCEL 300
Db      241 FCYLVITIRTLQARNPERKAIKVIIVAVVFIIVQLPYNGVLAQTVAENFITSSTCEL 300
Qy      301 SKQNLAIADVTYSLACVRCVNPFLYAFIYGVFRNDIFKLFRDLGCLSGEQLRQMSSCRH 360
Db      301 SKQNLAIADVTYSLACVRCVNPFLYAFIYGVFRNDIFKLFRDLGCLSGEQLRQMSSCRH 360
Qy      361 IRRSSMSVEAETTTTFSP 378
Db      361 IRRSSMSVEAETTTTFSP 378

```

RESULT 8
AAB50859
ID AAB50859 standard; protein; 378 AA.

```

AC      AAB50859;
XX
XX      16-MAR-2001 (first entry)
DT
XX      Human CCR7.
DE
XX
XX      Human; chemokine receptor 7; CCR7; chemokine beta-9; Ckbeta-9; allergy;
KW      autoimmune disease; ischaemia; atherosclerosis; cancer;
KW      chronic inflammatory disorder; organ transplant; tissue graft;
KW      chronic myelogenous leukaemia; infection.
XX

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OS      Homo sapiens.
XX
XX      US6153441-A.
XX
XX      28-NOV-2000.
PD
XX
XX      17-FEB-1999; 99US-00251545.
PF
XX      17-FEB-1998; 98US-0074883P.
PR
XX      (SMIK ) SMITHKLINE BEECHAM CORP.
PA
XX      Appelbaum ER, White JR, Sarau HM;
XX      WPI; 2001-049151/06.
DR
XX
XX      Identifying agonists or antagonists of interaction between human protein,
PT      chemokine beta-9 and human CC chemokine receptor 7, by contacting cell
PT      expressing receptor with test compound.
XX
XX      Claim 1; Fig 1; 20pp; English.
PS

```

The present sequence is human chemokine receptor 7 (CCR7), a cellular receptor for chemokine beta-9 (Ckbeta-9). The sequence may be used in a method for discovering agonists and antagonists of the interaction between Ckbeta-9 and CCR7. A cell expressing CCR7 polypeptide on its surface, associated with a component capable of providing a detectable signal in response to binding of Ckbeta-9, is contacted with a compound in the presence of labelled or unlabelled Ckbeta-9. The compound is identified as an agonist/antagonist by determining whether it activates

CC or inhibits the detectable signal. The method is useful for identifying CC agonists and antagonists of the interaction between Ckbeta-9 and CCR7 CC which are useful for treating diseases including allergic disorders, CC autoimmune diseases, ischaemia/reperfusion injury, development of CC atherosclerotic plaques, cancer, chronic inflammatory disorders, chronic CC rejection of transplanted organs or tissue grafts, chronic myelogenous CC leukaemia, and infection by HIV and other pathogens

XX Sequence 378 AA;

Query Match 99.2%; Score 1907; DB 4; Length 378;
Beet Local Similarity 99.2%; Pred. No. 9.1e-205;
Matches 375; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

Qy      1 MDLGRKMSVLLVALLVIFQVCLCODEVTDYIGDNTVDYTLFSLCSKKQVRNFKAMF 60
Db      1 MDLGRKMSVLLVALLVIFQVCLCODEVTDYIGDNTVDYTLFSLCSKKQVRNFKAMF 60
Qy      61 LPIMYSIICFVGLGNGLVVLTYYIFKRLKTMTDYTLNLAVADILFLTLPEFMAVSAK 120
Db      61 LPIMYSIICFVGLGNGLVVLTYYIFKRLKTMTDYTLNLAVADILFLTLPEFMAVSAK 120
Qy      121 SWFGVHFCKLIFAIYKMSFSGMILLICISIDRYVAIVQAVSAHRHARVLLISKSCV 180
Db      121 SWFGVHFCKLIFAIYKMSFSGMILLICISIDRYVAIVQAVSAHRHARVLLISKSCV 180
Qy      181 GSAILATVLSIPELLYSDLRSSSEQAMRCSLITEHVEAFITIQVAVWIGFVPLLAMS 240
Db      181 GIMILATVLSIPELLYSDLRSSSEQAMRCSLITEHVEAFITIQVAVWIGFVPLLAMS 240
Qy      241 FCYLVITIRTLQARNPERKAIKVIIVAVVFIIVQLPYNGVLAQTVAENFITSSTCEL 300
Db      241 FCYLVITIRTLQARNPERKAIKVIIVAVVFIIVQLPYNGVLAQTVAENFITSSTCEL 300
Qy      301 SKQNLAIADVTYSLACVRCVNPFLYAFIYGVFRNDIFKLFRDLGCLSGEQLRQMSSCRH 360
Db      301 SKQNLAIADVTYSLACVRCVNPFLYAFIYGVFRNDIFKLFRDLGCLSGEQLRQMSSCRH 360
Qy      361 IRRSSMSVEAETTTTFSP 378
Db      361 IRRSSMSVEAETTTTFSP 378

```

RESULT 9
AAU91230
ID AAU91230 standard; protein; 378 AA.
AAU91230;
18-JUN-2002 (first entry)

Human 7 transmembrane domain receptor V31 #2.
Human; 7 transmembrane domain receptor; 7TM; antiinflammatory;
immunomodulatory; immunological disease; inflammation;
familial breast cancer; von Hippel-Lindau syndrome;
thyroid hormone resistance; small cell cancer of the lung;
pseudo-Zellweger syndrome; hypoprote thrombinaemia; dysprothrombinaemia.

```

OS      Homo sapiens.
XX
XX      US6348574-B1.
XX
XX      19-FEB-2002.
PD
XX
XX      01-JUN-1998; 98US-00088337.
PF
XX      17-NOV-1992; 92US-00977452.
PR      17-NOV-1993; 93US-00153848.
PR      17-MAY-1994; 94US-00245242.
XX
XX      (ICOS-) ICOS CORP.
PA
XX

```

PI Godioka R, Gray PW, Schweickart VL;
XX WPI; 2002-266543/31.
DR N-PSDB; ABK54236.
XX
XX
PT New seven transmembrane receptor polypeptide R2, useful for producing
PT antibodies capable of modulating ligand/receptor binding reactions
PT involved in in vivo immunological and/or inflammatory events.
PS Example 3; Col 41-44; 61pp; English.
XX
XX The invention relates to a purified and isolated R2 seven transmembrane
XX (7TM) receptor. Also included are an anti-R2 antibody, a hybridoma
XX producing the antibody, antigenic peptide fragments of R2, an antiserum
XX produced by immunising a mammal with a composition comprising R2 or its
XX fragment, where the fragment comprises at least one R2 extracellular or
XX intracellular domain, and obtaining antiserum from the mammal after the
XX immunising step, where the antiserum contains antibodies that bind to the
XX R2 7TM receptor, a polynucleotide encoding 7TM receptor R2 and a host
XX cell stably transformed or transfected with the polynucleotide allowing
XX the expression of R2 in the host cell. The antibody is useful for
XX modulating ligand/antigen binding of a R2 7TM receptor, especially
XX those ligand/receptor binding reactions involved in immunological and/or
XX inflammatory events in vivo. R2 is useful for producing antibodies. The
XX antibody is useful for immunisation to generate anti-idiotypic
XX antibodies, for purifying R2 polypeptides, for identifying cells
XX producing the polypeptides on their surfaces and for the detection and
XX quantification of 7TM receptors on cell surfaces and in fluids. The
XX polynucleotide is useful in DNA/RNA hybridisation assays to detect the
XX capacity of cells to synthesise a 7TM receptor. The host cell is useful
XX for large scale production of 7TM receptors, and in assays for
XX identifying antagonist or agonists of 7TM receptor binding. Other 7TM
XX receptors isolated in this study include V31 (located on chromosome 17q12
XX -21.2, associated with familial breast cancer), V28 (chromosome 3p21-ter,
XX associated with von Hippel-Lindau syndrome, thyroid hormone resistance,
XX small cell cancer of the lung and pseudo-Zellweger syndrome), R20
XX (chromosome 11 p11-p13 associated with hypoproteinaemia and
XX dysprothrombinaemia), V112 and R12. The present sequence is a 7TM
XX receptor of the invention
SQ
Sequence 378 AA;
Query Match 99.2%; Score 1907; DB 5; Length 378;
Best Local Similarity 99.2%; Pred. No. 9.1e-205;
Matches 375; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 1 MDLGRPMKSVLVALLVIFQVCLCODEVTDYIGNTTYDYLTFESLCKKQVRNFKAMP 60
DB 1 MDLGRPMKSVLVALLVIFQVCLCODEVTDYIGNTTYDYLTFESLCKKQVRNFKAMP 60
OY 61 LPIMTSIICFVGLNGVLVLTYYIFPKRLKMTDTYLLNLAVADILFLLTLPFMAYSAK 120
DB 61 LPIMTSIICFVGLNGVLVLTYYIFPKRLKMTDTYLLNLAVADILFLLTLPFMAYSAK 120
OY 121 SWFGVHFCKLIPAIYKMSFFSGMLLLCISIDRYVAIVQAVSAHRHRAVLLISLSCV 180
DB 121 SWFGVHFCKLIPAIYKMSFFSGMLLLCISIDRYVAIVQAVSAHRHRAVLLISLSCV 180
OY 181 GSAILATVLSIBELYSIDLRSSSEQAKCSLITHEVEAFITIOVAQWIGFVLPILAMS 240
DB 181 GSAILATVLSIBELYSIDLRSSSEQAKCSLITHEVEAFITIOVAQWIGFVLPILAMS 240
OY 191 GIWILATVLSIBELYSIDLRSSSEQAKCSLITHEVEAFITIOVAQWIGFVLPILAMS 240
DB 241 FCYLVIIIRTLQARNFERKAIKVIIVAVVVEIVFOLPYNGLVLAQTVANFNITSSTCEL 300
OY 301 SKQNLIAVDVYSLACVRCVNPFLYAFIGVFRNDIFKLFDLGLCLSGEQRLQWSSCH 360
DB 301 SKQNLIAVDVYSLACVRCVNPFLYAFIGVFRNDIFKLFDLGLCLSGEQRLQWSSCH 360
OY 361 IRRSSMSVEAETTTTSP 378
DB 361 IRRSSMSVEAETTTTSP 378

RESULT 10
ID ABP97730
ABP97730 standard; protein; 378 AA.
XX
XX
AC ABP97730;
XX
XX 28-MAY-2003 (first entry)
DE Amino acid sequence of human chemokine receptor CCR7.
XX
XX Human; chemokine receptor; CCR7; viral infection; surface protein;
XX respiratory virus infection; respiratory syncytial virus infection;
XX RSV infection; bronchiolitis; bronchitis; pneumonia; asthma.
OS Homo sapiens.
XX
XX WO2003014153-A2.
XX
XX 20-FEB-2003.
XX
XX 12-AUG-2002; 2002WO-CA001248.
XX
XX 10-AUG-2001; 2001US-0311088P.
XX
XX (TOP1-) TOPIGEN PHARM INC.
XX
XX Renzi P, Zemzouni K;
XX
XX WPI; 2003-256541/25.
XX
XX N-PSDB; ABK68883.
PT Modulating viral infection of a cell, for treating or preventing
PT respiratory virus infections, bronchitis, pneumonia or asthma, by
PT modulating a binding interaction between a cell chemokine-receptor and a
PT surface protein of the virus.
XX
XX
XX Disclosure; Page 106-107; 120pp; English.
XX
XX
XX The present sequence represents human chemokine receptor CCR7. The
XX specification describes a method for modulating viral infection of a
XX cell. The method comprises modulating a binding interaction between a
XX cell chemokine-receptor and a surface protein of the virus. The proviso
XX is that the cell chemokine-receptor is not CX3CR1 and that the virus is
XX not HIV. The method is useful for treating or preventing respiratory
XX virus infection in vertebrates, more particularly respiratory syncytial
XX virus (RSV) infections, and related diseases, e.g. bronchiolitis,
XX bronchitis, pneumonia or asthma
SQ
Sequence 378 AA;
Query Match 99.2%; Score 1907; DB 6; Length 378;
Best Local Similarity 99.2%; Pred. No. 9.1e-205;
Matches 375; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 1 MDLGRPMKSVLVALLVIFQVCLCODEVTDYIGNTTYDYLTFESLCKKQVRNFKAMP 60
DB 1 MDLGRPMKSVLVALLVIFQVCLCODEVTDYIGNTTYDYLTFESLCKKQVRNFKAMP 60
OY 61 LPIMTSIICFVGLNGVLVLTYYIFPKRLKMTDTYLLNLAVADILFLLTLPFMAYSAK 120
DB 61 LPIMTSIICFVGLNGVLVLTYYIFPKRLKMTDTYLLNLAVADILFLLTLPFMAYSAK 120
OY 121 SWFGVHFCKLIPAIYKMSFFSGMLLLCISIDRYVAIVQAVSAHRHRAVLLISLSCV 180
DB 121 SWFGVHFCKLIPAIYKMSFFSGMLLLCISIDRYVAIVQAVSAHRHRAVLLISLSCV 180
OY 181 GSAILATVLSIBELYSIDLRSSSEQAKCSLITHEVEAFITIOVAQWIGFVLPILAMS 240
DB 181 GSAILATVLSIBELYSIDLRSSSEQAKCSLITHEVEAFITIOVAQWIGFVLPILAMS 240
OY 191 GIWILATVLSIBELYSIDLRSSSEQAKCSLITHEVEAFITIOVAQWIGFVLPILAMS 240
DB 241 FCYLVIIIRTLQARNFERKAIKVIIVAVVVEIVFOLPYNGLVLAQTVANFNITSSTCEL 300

Db 241 FCYLVITITLLQANRFRNKAIKVIIAAVVVFIVFQLPYNGVLAQTVAANFNTTSTCEL 300
QY 301 SKQINIAVDVTVSLACVRCVCPNPLFYAFIVGKFRNDIFKLFRDGLCSOEQLRQWSSCRH 360
Db 301 SKQINIAVDVTVSLACVRCVCPNPLFYAFIVGKFRNDIFKLFRDGLCSOEQLRQWSSCRH 360
QY 361 IRRSSMSVEAEITTTTFFSP 378
Db 361 IRRSSMSVEAEITTTTFFSP 378
RESULT 11
ABP81793
ID ABP81793 standard; protein, 378 AA.
AC ABP81793;
DT 04-MAR-2003 (first entry)
DE Human C-C chemokine receptor 7 protein SEQ ID NO:68.
KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer.
XX Homo sapiens.
XX OS
XX MO200261087-A2.
XX PN 08-AUG-2002.
XX PD 19-DEC-2001; 2001MO-US050107.
XX PF 19-DEC-2000; 2000US-0257144P.
XX PR 19-DEC-2000; 2000US-0257144P.
XX PA (LIFE-) LIFESPAN BIOSCIENCES INC.
XX PI Burner GC, Roush CL, Brown JP;
XX DR MPI; 2003-046718/04.
XX DR N-PSDB; AB242637.
XX PT New isolated antigenic peptides e.g., for G protein-coupled receptors
XX PT (GPCR), useful for diagnosing and designing drugs for treating conditions
XX PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
XX PT autoimmune diseases.
XX PS Disclosure; Fig 1; 523pp; English.
XX PS The present invention describes antigenic peptides (I) comprising: (a)
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular G
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity or
CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related diseases, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC

CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. AB242523 to AB242669 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention
XX
XX Sequence 378 AA:
Query Match 99.2%; Score 1907; DB 6; Length 378;
Best Local Similarity 99.2%; Pred. No. 9.1e-205;
Matches 375; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MDLQKPMKSVLVALLVIFQVCLCODEVTDDYIGDNTVDYTLFESLCSKKDVRNFKAMP 60
Db 1 MDLQKPMKSVLVALLVIFQVCLCODEVTDDYIGDNTVDYTLFESLCSKKDVRNFKAMP 60
QY 61 LPIMYSIICFVGLGNGLVVLTYYFKRLKMTDTYLLNLAVADILFLTLTLPMAVSAK 120
Db 61 LPIMYSIICFVGLGNGLVVLTYYFKRLKMTDTYLLNLAVADILFLTLTLPMAVSAK 120
QY 121 SWFGVHFCKLIPIAYKMSFPGMILLICISIDRYVAIVQAVSAHRHARVLLISKSCV 180
Db 121 SWFGVHFCKLIPIAYKMSFPGMILLICISIDRYVAIVQAVSAHRHARVLLISKSCV 180
QY 181 GSALATATLSIPELLSPDLORSSSEQAMRCSLIEHVEAFITIOVAQWVIGFLVPLAMS 240
Db 181 GIWILATVLSIPELLSPDLORSSSEQAMRCSLIEHVEAFITIOVAQWVIGFLVPLAMS 240
QY 241 FCYLVITITLLQANRFRNKAIKVIIAAVVVFIVFQLPYNGVLAQTVAANFNTTSTCEL 300
Db 241 FCYLVITITLLQANRFRNKAIKVIIAAVVVFIVFQLPYNGVLAQTVAANFNTTSTCEL 300
QY 301 SKQINIAVDVTVSLACVRCVCPNPLFYAFIVGKFRNDIFKLFRDGLCSOEQLRQWSSCRH 360
Db 301 SKQINIAVDVTVSLACVRCVCPNPLFYAFIVGKFRNDIFKLFRDGLCSOEQLRQWSSCRH 360
QY 361 IRRSSMSVEAEITTTTFFSP 378
Db 361 IRRSSMSVEAEITTTTFFSP 378
RESULT 12
ADC22593
ID ADC22593 standard; protein, 378 AA.
XX
XX AC ADC22593;
XX AC 18-DEC-2003 (first entry)
XX DT Human G protein-coupled receptor (GPCR) polypeptide #21.
XX DE Human G protein-coupled receptor (GPCR) polypeptide #21.
XX KW Human; G protein-coupled receptor; GPCR; transmembrane-6 region; TM6;
XX KW intracellular-3 region; IC3; receptor.
XX OS Homo sapiens.
XX OS US6555339-B1.
XX PN 29-APR-2003.
XX PD 13-OCT-1998; 98US-00170496.
XX PF 14-APR-1997; 97US-00839449.
XX PR 14-APR-1998; 98US-00060188.
XX PR 26-JUN-1998; 98US-0090783P.
XX PR 07-AUG-1998; 98US-0095677P.
XX PA (AREN-) ARENA PHARM INC.

Query Match	Best Local Match	Score	DB	Length	Matches	Conservative	1	Mismatches	2	Indels	0	Gaps	0
QY	1 MDLGRKMSVLVALLVIFQVCLACDEVTDDYIGDNTTYDYLTFESLSCKDQVRNFKAMF	99.2%	1907	378	99.2%	1	1	205	2	0	0	0	0
DB	1 MDLGRKMSVLVALLVIFQVCLACDEVTDDYIGDNTTYDYLTFESLSCKDQVRNFKAMF	99.2%	1907	378	99.2%	1	1	205	2	0	0	0	0
QY	61 LPIWYSIICFVGLLNGVLVLTYYIFPKRLKMTDYYLNLAVADILFLTLTFPMWYSAK	99.2%	1907	378	99.2%	1	1	205	2	0	0	0	0
DB	61 LPIWYSIICFVGLLNGVLVLTYYIFPKRLKMTDYYLNLAVADILFLTLTFPMWYSAK	99.2%	1907	378	99.2%	1	1	205	2	0	0	0	0
QY	121 SWFSEVNHCKLIFATYKMSFSEGMILLICISIDRYAALYQAVSARHRRARVLLISLSCV	99.2%	1907	378	99.2%	1	1	205	2	0	0	0	0
DB	121 SWFSEVNHCKLIFATYKMSFSEGMILLICISIDRYAALYQAVSARHRRARVLLISLSCV	99.2%	1907	378	99.2%	1	1	205	2	0	0	0	0
QY	181 GSALATATLSTPELILYSDLDQRSSSOAMRCSLITEHVEAFITTOVAQWITGFLVPLAMS	99.2%	1907	378	99.2%	1	1	205	2	0	0	0	0
DB	181 GSALATATLSTPELILYSDLDQRSSSOAMRCSLITEHVEAFITTOVAQWITGFLVPLAMS	99.2%	1907	378	99.2%	1	1	205	2	0	0	0	0
QY	241 FCYLVITIRTLQARNFERNKAIKVIAVAVVIFVQLPNGVLAQTVANFNTISTCEL	99.2%	1907	378	99.2%	1	1	205	2	0	0	0	0
DB	241 FCYLVITIRTLQARNFERNKAIKVIAVAVVIFVQLPNGVLAQTVANFNTISTCEL	99.2%	1907	378	99.2%	1	1	205	2	0	0	0	0
QY	301 SKOLNIADVITYSLACVRCNPNLYAFIGVFRNDIFKLFQDLGCLSGEQLRWSSCRH	99.2%	1907	378	99.2%	1	1	205	2	0	0	0	0
DB	301 SKOLNIADVITYSLACVRCNPNLYAFIGVFRNDIFKLFQDLGCLSGEQLRWSSCRH	99.2%	1907	378	99.2%	1	1	205	2	0	0	0	0
QY	361 IRRSSMSVEAETTTTFFSP	99.2%	1907	378	99.2%	1	1	205	2	0	0	0	0
DB	361 IRRSSMSVEAETTTTFFSP	99.2%	1907	378	99.2%	1	1	205	2	0	0	0	0

[illegible]

Db 301 SKQINAIADVITYSLACVRCVNPFLYAFIVGFPRNDLFKLFKDGLCSOEOLRQWSSCRH 360
QY 361 IRRSSMSVEAETTTTFFSP 378
Db 361 IRRSSMSVEAETTTTFFSP 378
RESULT 14
ADH13199
ID ADH13199 standard; protein; 378 AA.
XX
AC ADH13199;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human malignant neoplasia-related protein Segid48.
XX
KW malignant neoplasia; cytostatic; breast cancer; ovarian cancer;
KW gastric cancer; colon cancer; oesophageal cancer; mesenchymal cancer;
KW bladder cancer; non-small cell lung cancer; human.
XX
OS Homo sapiens.
XX
PN EP1365034-A2.
XX
PD 26-NOV-2003.
XX
PF 09-MAY-2003; 2003EP-00010447.
XX
PR 21-MAY-2002; 2002EP-00010291.
XX
PR 13-FEB-2003; 2003EP-00003112.
XX
PA (FARB) BAYER AG.
XX
PI Wirtz R, Munnes M, Kallabis H;
XX
DR WPI; 2004-073279/08.
XX
DR N-PSDB; ADH13173.
XX
PT Predicting, diagnosing or prognosing malignant neoplasia by detecting at
PT least two markers, where the markers are genes from one or more
PT chromosomal regions altered in malignant neoplasia.
XX
PS Claim 11; SEQ ID NO 48; 267bp; English.
XX
CC This invention relates to a novel method for the prediction, diagnosis,
CC or prognosis of malignant neoplasia by the detection of at least two
CC markers. The invention may also be useful for the development of
CC cyrostatic compounds through the regulation of the expression of a gene
CC or activity of a protein associated with malignant neoplasia. The method
CC is useful for prediction, diagnosis or prognosis of malignant neoplasia
CC such as breast cancer, ovarian cancer, gastric cancer, colon cancer,
CC oesophageal cancer, mesenchymal cancer, bladder cancer or non-small cell
CC lung cancer. The polynucleotides and polypeptides defined in the
CC specification, antisense polynucleotides targeting the polynucleotides,
CC antibodies targeting either one of the polynucleotides or polypeptides,
CC and compounds identified by the screening methods are useful for
CC preventing or treating malignant neoplasia. The disease treated is
CC preferably breast cancer. The present sequence is that of a human
CC malignant neoplasia-related protein which may be used in the method of
CC the invention.
XX
SQ Sequence 378 AA;
Query Match 99.2%; Score 1907; DB 8; Length 378;
Best Local Similarity 99.2%; Pred. No. 9.1e-205;
Matches 375; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 61 LPIMSIICFVGLGNGLVLTLYIFPKLKTMTDTYLLNLAVADILFLTLTFPMAYSAK 120
QY 121 SWFGVHFCKLIIPAIYKMSFFSGMLLLCISIDRYVAIVQAVSARRHARVLLISKLSKV 180
Db 121 SWFGVHFCKLIIPAIYKMSFFSGMLLLCISIDRYVAIVQAVSARRHARVLLISKLSKV 180
QY 181 GSAILATVLSIPELLYSDLQRRSSBQAMRCSLITHEVAFITTIQVAVNIGFVPLAMS 240
Db 181 GIWILATVLSIPELLYSDLQRRSSBQAMRCSLITHEVAFITTIQVAVNIGFVPLAMS 240
QY 241 FCYLVITRTLLQARNPEENKAIKVIIVAVVFIVFQLPYNGVLAQVATANNTISSTCEL 300
Db 241 FCYLVITRTLLQARNPEENKAIKVIIVAVVFIVFQLPYNGVLAQVATANNTISSTCEL 300
QY 301 SKQINAIADVITYSLACVRCVNPFLYAFIVGFPRNDLFKLFKDGLCSOEOLRQWSSCRH 360
Db 301 SKQINAIADVITYSLACVRCVNPFLYAFIVGFPRNDLFKLFKDGLCSOEOLRQWSSCRH 360
QY 361 IRRSSMSVEAETTTTFFSP 378
Db 361 IRRSSMSVEAETTTTFFSP 378
RESULT 15
ADO29231
ID ADO29231 standard; protein; 378 AA.
XX
AC ADO29231;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human GPCR CCR7, SEQ ID NO:332.
XX
KW G protein-coupled receptor; GPCR; drug screening; diagnosis;
KW transgenic mouse; neurological disorder; adrenal gland disorder;
KW colon disorder; intestinal disorder; cardiovascular disorder;
KW muscular disorder; blood disorder; immune disorder; bone disorder;
KW joint disorder; metabolic disorder; nutritive disorder; cancer;
KW kidney disorder; liver disorder; lung disorder; breast disorder;
KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
KW chymus disorder; thyroid disorder; antiparkinsonian; antianitic;
KW cytostatic; antiinflammatory; vasotrophic; antianginal; antiarhythmic;
KW CNS; central nervous system; respiratory; antidiabetic; antidiabetic;
KW vincristine; hepatotropic; antibacterial; antianemic; antiepileptic;
KW dermatological; antitumor; antithyroid; antiallergic; anorectic;
KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
KW receptor.
XX
OS Homo sapiens.
XX
PN WO2004040000-A2.
XX
PD 13-MAY-2004.
XX
PF 09-SEP-2003; 2003WO-US028226.
XX
PR 09-SEP-2002; 2002US-0409303P.
XX
PR 09-APR-2003; 2003US-0461329P.
XX
PA (PRIM-) PRIMAL INC.
XX
PI Galtanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
XX
PI Madisen L, McIlwain KU, Pavlova MN, Vassilatis D, Zeng H;
XX
DR WPI; 2004-390329/36.
XX
DR N-PSDB; ADO29834.
XX
PT Novel mammalian G protein coupled receptors, useful for identifying
PT compounds that modulates diagnosing and treating disease condition
PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
PT pectoris, Parkinson's disease.

XX Claim 151; SEQ ID NO 332; 542pp; English.

CC The invention relates to human and mouse G protein-coupled receptors
CC (GPCRs) and nucleic acids encoding them. The invention also relates to
CC sequences at least 90% identical to the GPCR proteins and nucleic acids
CC of the invention; methods of treating, preventing or diagnosing diseases
CC associated with GPCRs of the invention; methods of screening for
CC compounds useful in the treatment of GPCR-related diseases; a transgenic
CC mouse comprising a GPCR gene of the invention; a mouse comprising a
CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
CC from the transgenic mice; kits comprising several mice, each of which has
CC a mutation in a different GPCR gene of the invention; and kits comprising
CC probes which hybridize to GPCR polynucleotides of the invention. The
CC invention further discloses variants of the GPCR polypeptides and vectors
CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
CC be used in the diagnosis, treatment or prevention of a wide variety of
CC diseases including neurological disorders (e.g., Alzheimer's disease,
CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
CC disorders of the adrenal gland; disorders of the colon or intestine
CC (e.g., Crohn's disease, diarrhea, food poisoning or irritable bowel
CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
CC myocardial infarction); muscular disorders; blood disorders (e.g.,
CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
CC thyroid (e.g., cancers). The present sequence represents a GPCR of the
CC invention. Note: The full sequence data for this patent did not form part
CC of the printed specification; those sequences not shown were obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX
SQ Sequence 378 AA;

Query Match 99.2%; Score 1907; DB 8; Length 378;
Best Local Similarity 99.2%; Pred. No. 9.1e-205;
Matches 375; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDLGRKMSVLLVALLVITVQVCLCODEVDDYIGDNTTVDYTLFESLCSKKDYRNKAF 60
DB 1 MDLGRKMSVLLVALLVITVQVCLCODEVDDYIGDNTTVDYTLFESLCSKKDYRNKAF 60
QY 61 LPTMSIICFVGLGNGLVVLTIVYFKRKTMTDTYLLNLA VADILFLTLFPMAISA 120
DB 61 LPTMSIICFVGLGNGLVVLTIVYFKRKTMTDTYLLNLA VADILFLTLFPMAISA 120
QY 121 SWVFGVHFKLIFAIYKMSFSGMLLLCISIDRYVAIVQAVSAHRHRAVLLISKLS 180
DB 121 SWVFGVHFKLIFAIYKMSFSGMLLLCISIDRYVAIVQAVSAHRHRAVLLISKLS 180
QY 181 GSAILATVLSIPPELLYSIDLRSSSEQMRCSLITEHVEAFITTVQAVMTIGFLVPL 240
DB 181 GSAILATVLSIPPELLYSIDLRSSSEQMRCSLITEHVEAFITTVQAVMTIGFLVPL 240
QY 241 FCYLVITRTLLQARNERNKAIVITAAVVVFVFPOLPYNGVLAQTVANFNITSS 300
DB 241 FCYLVITRTLLQARNERNKAIVITAAVVVFVFPOLPYNGVLAQTVANFNITSS 300
QY 301 SKQLNIAYDVTVSLACVRCVNPFLYAFIGVKFRNDIFKLFKDLGCLSGEQLRQWSS 360
DB 301 SKQLNIAYDVTVSLACVRCVNPFLYAFIGVKFRNDIFKLFKDLGCLSGEQLRQWSS 360
QY 361 IRRSSMSVEAETTTTSP 378
DB 361 IRRSSMSVEAETTTTSP 378

Search completed: February 25, 2005, 02:19:57
Job time : 168 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: February 25, 2005, 02:15:02 ; Search time 43 Seconds
(without alignments)
656,217 Million cell updates/sec

Title: US-10-749-990-2

Perfect score: 1922

Sequence: 1 MDLGRKMSVLLVALLVIFQ.....RHRRSSMSVETTTTSP 378

Scoring table: BLOSUM62

Searched: 513545 seqs, 7464964 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/aa/5A_COMB.pep.*
- 2: /cgn2_6/prodata/1/aa/5B_COMB.pep.*
- 3: /cgn2_6/prodata/1/aa/6A_COMB.pep.*
- 4: /cgn2_6/prodata/1/aa/6B_COMB.pep.*
- 5: /cgn2_6/prodata/1/aa/PCTUS_COMB.pep.*
- 6: /cgn2_6/prodata/1/aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1932	100.0	378	1	US-08-383-750-2
2	1922	100.0	378	1	US-08-383-751A-2
3	1922	100.0	378	3	US-08-352-678-2
4	1922	100.0	378	4	US-09-045-583-49
5	1922	100.0	378	4	US-09-534-185-49
6	1922	100.0	378	4	US-09-536-954-2
7	1922	100.0	378	4	US-09-529-583B-2
8	1922	100.0	378	4	US-09-721-341-7
9	1922	100.0	378	4	US-09-721-495B-7
10	1922	100.0	378	5	PCT-US93-09636-2
11	1922	99.2	378	1	US-08-153-848-15
12	1907	99.2	378	3	US-09-299-843A-15
13	1907	99.2	378	3	US-09-251-545-1
14	1907	99.2	378	3	US-09-088-337B-15
15	1907	99.2	378	4	US-09-170-496D-74
16	1907	99.2	378	5	PCT-US93-11153-15
17	1900	98.9	378	4	US-09-170-496D-204
18	1814	94.4	410	1	US-08-153-848-7
19	1814	94.4	410	3	US-09-299-843A-7
20	1814	94.4	410	3	US-09-088-337B-7
21	1814	94.4	410	5	PCT-US93-11153-7
22	1813	94.3	358	1	US-08-153-848-19
23	1813	94.3	358	3	US-09-299-843A-19
24	1813	94.3	358	3	US-09-088-337B-19
25	1813	94.3	358	5	PCT-US93-11153-19
26	1795.5	93.4	361	2	US-08-902-294-2
27	1795.5	93.4	361	3	US-09-178-637-2

28	1696	88.2	378	3	US-09-299-843A-66	Sequence 66, App1
29	1696	88.2	378	3	US-09-088-337B-66	Sequence 66, App1
30	1602.5	83.4	359	1	US-08-153-848-24	Sequence 24, App1
31	1602.5	83.4	359	3	US-09-299-843A-24	Sequence 24, App1
32	1602.5	83.4	359	3	US-09-088-337B-24	Sequence 24, App1
33	1602.5	83.4	359	5	PCT-US93-11153-24	Sequence 24, App1
34	758.5	39.5	357	3	US-09-266-464-2	Sequence 2, App1
35	758.5	39.5	357	4	US-09-170-496D-24	Sequence 24, App1
36	758.5	39.5	357	4	US-09-952-385-2	Sequence 2, App1
37	758.5	39.5	369	4	US-09-721-341-6	Sequence 6, App1
38	758.5	39.5	369	4	US-09-721-495B-6	Sequence 6, App1
39	758.5	39.5	371	4	US-09-949-016-11223	Sequence 11223, A
40	753.5	39.2	357	4	US-09-170-496D-176	Sequence 176, App
41	753.5	39.2	369	4	US-09-826-509-481	Sequence 481, App
42	707.5	36.8	374	3	US-09-045-583-48	Sequence 48, App1
43	707.5	36.8	374	4	US-09-534-185-48	Sequence 48, App1
44	704.5	36.7	374	4	US-09-721-341-8	Sequence 8, App1
45	704.5	36.7	374	4	US-09-721-495B-8	Sequence 8, App1

ALIGNMENTS

RESULT 1
US-08-383-750-2
Sequence 2, Application US/08383750
Patent No. 5744301
GENERAL INFORMATION:
APPLICANT: Birkenbach, Mark
TITLE OF INVENTION: Epstein Barr Virus Induced Genes
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESS: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, N.W.,
CITY: Suite 600
STATE: Washington
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/383,750
FILING DATE: Herewith
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Fox, Samuel, L.
REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 0627.3300001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-383-750-2

Query Match 100.0%; Score 1922; DB 1; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.7e-153; Indels 0; Gaps 0;
Matches 378; Conservative 0; Mismatches 0;

QY 1 MDLGRKMSVLLVALLVIFQVCLCODEVDYDYGNTTVDTLLFESLCKKODRNFKAHF 60
DB 1 MDLGRKMSVLLVALLVIFQVCLCODEVDYDYGNTTVDTLLFESLCKKODRNFKAHF 60
QY 61 LPIWYIIFVGLGNGLVLLTYTYRKIKMTDTYLLNLAVADIIFLLTLPFWYSAK 120

Db 61 LPIMYSICFVGLNGVLLVLTYYFKRLKMTDTYLLNLAVADILFLTLTPEFMAVSAK 120
QY 121 SWFGVHFCKLIIPAIYKMSFSGMLLLCISIDRYVAIVQAVSAHRHARVLLISKSCV 180
Db 121 SWFGVHFCKLIIPAIYKMSFSGMLLLCISIDRYVAIVQAVSAHRHARVLLISKSCV 180
QY 181 GSAILATVLSIPELLYSIDLQRSSSEQAMRCSLITHEVAFITTIQVAVNIGFLVPLLMS 240
Db 181 GSAILATVLSIPELLYSIDLQRSSSEQAMRCSLITHEVAFITTIQVAVNIGFLVPLLMS 240
QY 241 FCYLVITRLQARPERKAIKVIIVVVFIVFQLPYNGVLAQTVANFNITSSTCEL 300
Db 241 FCYLVITRLQARPERKAIKVIIVVVFIVFQLPYNGVLAQTVANFNITSSTCEL 300
QY 301 SKQLNIADVITYSLACVRCVNPFLYAFIGVFRNDIFKLPDGLCGLSQEQRLQWSSCGH 360
Db 301 SKQLNIADVITYSLACVRCVNPFLYAFIGVFRNDIFKLPDGLCGLSQEQRLQWSSCGH 360
QY 361 IRRSSMSVAEETTTTTFSP 378
Db 361 IRRSSMSVAEETTTTTFSP 378

RESULT 2

US-08-383-751A-2
Sequence 2, Application US/08383751A
Patent No. 5753516
GENERAL INFORMATION:
APPLICANT: Heagy, Wyrta E.
APPLICANT: Flinberg, Robert W.
TITLE OF INVENTION: Identification and Uses of Opioid
TITLE OF INVENTION: Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: US
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/383,751A
FILING DATE: 03-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: DFCI:001/WIM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-383-751A-2

Query Match 100.0%; Score 1922; DB 1; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.7e-153;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLGRKMSVLLVALLVIFQVCLCODEVTDDYIGDNTVDYTLFESLCSKKQVRNPKAF 60
Db 1 MDLGRKMSVLLVALLVIFQVCLCODEVTDDYIGDNTVDYTLFESLCSKKQVRNPKAF 60
QY 61 LPIMYSICFVGLNGVLLVLTYYFKRLKMTDTYLLNLAVADILFLTLTPEFMAVSAK 120

Db 61 LPIMYSICFVGLNGVLLVLTYYFKRLKMTDTYLLNLAVADILFLTLTPEFMAVSAK 120
QY 121 SWFGVHFCKLIIPAIYKMSFSGMLLLCISIDRYVAIVQAVSAHRHARVLLISKSCV 180
Db 121 SWFGVHFCKLIIPAIYKMSFSGMLLLCISIDRYVAIVQAVSAHRHARVLLISKSCV 180
QY 181 GSAILATVLSIPELLYSIDLQRSSSEQAMRCSLITHEVAFITTIQVAVNIGFLVPLLMS 240
Db 181 GSAILATVLSIPELLYSIDLQRSSSEQAMRCSLITHEVAFITTIQVAVNIGFLVPLLMS 240
QY 241 FCYLVITRLQARPERKAIKVIIVVVFIVFQLPYNGVLAQTVANFNITSSTCEL 300
Db 241 FCYLVITRLQARPERKAIKVIIVVVFIVFQLPYNGVLAQTVANFNITSSTCEL 300
QY 301 SKQLNIADVITYSLACVRCVNPFLYAFIGVFRNDIFKLPDGLCGLSQEQRLQWSSCGH 360
Db 301 SKQLNIADVITYSLACVRCVNPFLYAFIGVFRNDIFKLPDGLCGLSQEQRLQWSSCGH 360
QY 361 IRRSSMSVAEETTTTTFSP 378
Db 361 IRRSSMSVAEETTTTTFSP 378

RESULT 3

US-08-352-678-2
Sequence 2, Application US/08352678
Patent No. 6043351
GENERAL INFORMATION:
APPLICANT: Birkenbach, Mark
APPLICANT: Kieff, Elliott
TITLE OF INVENTION: EPSTEIN BARR VIRUS INDUCED GENES
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/352,678
FILING DATE: 30-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/980,518
FILING DATE: 25-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gates, Edward R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: B0801/7044
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-352-678-2

Query Match 100.0%; Score 1922; DB 3; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.7e-153;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLGRKMSVLLVALLVIFQVCLCODEVTDDYIGDNTVDYTLFESLCSKKQVRNPKAF 60

Db 1 MDLGRKMSVLLVALLVIFQVCLCODEVTDDYIGDNTTVDYTLFESLCSKQDVNRKAMP 60
Qy 61 LPIWTSIIICFVGLGNGLVLLTYIYFKRLKTMIDTYLLNLAVADILFLLTLPFWAASA 120
Db 61 LPIWTSIIICFVGLGNGLVLLTYIYFKRLKTMIDTYLLNLAVADILFLLTLPFWAASA 120
Qy 121 SWFGVHFCKLIPAIYKMSFFSGMLLLCISIDRYVAIVQAVSAHRRARVLLISKSCV 180
Db 121 SWFGVHFCKLIPAIYKMSFFSGMLLLCISIDRYVAIVQAVSAHRRARVLLISKSCV 180
Qy 181 GSAIIATVLSIPELVSDLRSSSEQAMRCSLITEHVAFTITQVQAWYIGFLVPLLA 240
Db 181 GSAIIATVLSIPELVSDLRSSSEQAMRCSLITEHVAFTITQVQAWYIGFLVPLLA 240
Qy 241 FCYLVIRTLQARNERNKAIKVIIVAVVFIQVLPNGVLAQTVANFNITSTCEL 300
Db 241 FCYLVIRTLQARNERNKAIKVIIVAVVFIQVLPNGVLAQTVANFNITSTCEL 300
Qy 301 SKQNLAYDVVTSIACVRCVNPFLYAFIGVKFRNDIFKLPDGLGCLSGOLRQSSCRH 360
Db 301 SKQNLAYDVVTSIACVRCVNPFLYAFIGVKFRNDIFKLPDGLGCLSGOLRQSSCRH 360
Qy 361 IRRSSMSVEAETTTTFSP 378
Db 361 IRRSSMSVEAETTTTFSP 378

RESULT 4

US-09-045-583-49
; Sequence 49, Application US/09045583
; Patent No. 6287805
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/045,583
; FILING DATE: 20-MAR-98
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNT-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-045-583-49

Query Match 100.0%; Score 1922; DB 3; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.7e-153;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDLGRKMSVLLVALLVIFQVCLCODEVTDDYIGDNTTVDYTLFESLCSKQDVNRKAMP 60
Db 1 MDLGRKMSVLLVALLVIFQVCLCODEVTDDYIGDNTTVDYTLFESLCSKQDVNRKAMP 60
Qy 61 LPIWTSIIICFVGLGNGLVLLTYIYFKRLKTMIDTYLLNLAVADILFLLTLPFWAASA 120
Db 61 LPIWTSIIICFVGLGNGLVLLTYIYFKRLKTMIDTYLLNLAVADILFLLTLPFWAASA 120
Qy 121 SWFGVHFCKLIPAIYKMSFFSGMLLLCISIDRYVAIVQAVSAHRRARVLLISKSCV 180
Db 121 SWFGVHFCKLIPAIYKMSFFSGMLLLCISIDRYVAIVQAVSAHRRARVLLISKSCV 180
Qy 181 GSAIIATVLSIPELVSDLRSSSEQAMRCSLITEHVAFTITQVQAWYIGFLVPLLA 240
Db 181 GSAIIATVLSIPELVSDLRSSSEQAMRCSLITEHVAFTITQVQAWYIGFLVPLLA 240
Qy 241 FCYLVIRTLQARNERNKAIKVIIVAVVFIQVLPNGVLAQTVANFNITSTCEL 300
Db 241 FCYLVIRTLQARNERNKAIKVIIVAVVFIQVLPNGVLAQTVANFNITSTCEL 300
Qy 301 SKQNLAYDVVTSIACVRCVNPFLYAFIGVKFRNDIFKLPDGLGCLSGOLRQSSCRH 360
Db 301 SKQNLAYDVVTSIACVRCVNPFLYAFIGVKFRNDIFKLPDGLGCLSGOLRQSSCRH 360
Qy 361 IRRSSMSVEAETTTTFSP 378
Db 361 IRRSSMSVEAETTTTFSP 378

RESULT 5

US-09-534-185-49
; Sequence 49, Application US/09534185
; Patent No. 6403767
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
; Hepahelical Receptor Superfamily and Uses
; Therefor
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/534,185
; FILING DATE: 24-Mar-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/045,583
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNT-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-09-534-185-49

Query Match 100.0%; Score 1922; DB 4; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.7e-153;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MDLGRPKMSVLLVALLVIFQVCLCODEVTDDYIGNTTVDYTLFESLCSKKQVRNFKAMF 60
DB 1 MDLGRPKMSVLLVALLVIFQVCLCODEVTDDYIGNTTVDYTLFESLCSKKQVRNFKAMF 60
QY 61 LPIWTSIIICFVGLLNGVLVLTYYIFKRLKTMPTDYLLNLAVADILFLTLTPEFMAVSAK 120
DB 61 LPIWTSIIICFVGLLNGVLVLTYYIFKRLKTMPTDYLLNLAVADILFLTLTPEFMAVSAK 120
QY 121 SWFEGVHFCKLIFAIYKMSFSGMLLLCISIDRYVAIVQAVSARHRRARVLLISKSCV 180
DB 121 SWFEGVHFCKLIFAIYKMSFSGMLLLCISIDRYVAIVQAVSARHRRARVLLISKSCV 180
QY 181 GSAIIATVLSIPELLYSDLRSSSEQARCSLITHEVAFTITIOVAVIGFLVPLAMS 240
DB 181 GSAIIATVLSIPELLYSDLRSSSEQARCSLITHEVAFTITIOVAVIGFLVPLAMS 240
QY 241 FCYLVIRTLQARNPERKAIKVIIAVVVFIVFQLPYNGVLAQTVANFNITSTCEL 300
DB 241 FCYLVIRTLQARNPERKAIKVIIAVVVFIVFQLPYNGVLAQTVANFNITSTCEL 300
QY 301 SKQINIAVDVYSLACVRCVNPFLYAFIGVFRNDIFLFDLGLCSOEOLRQWSSCRH 360
DB 301 SKQINIAVDVYSLACVRCVNPFLYAFIGVFRNDIFLFDLGLCSOEOLRQWSSCRH 360
QY 361 IRRSSMSVBAETTTTFSP 378
DB 361 IRRSSMSVBAETTTTFSP 378
```

RESULT 6

US-09-536-954-2
Sequence 2, Application US/09536954
Patent No. 6500926

GENERAL INFORMATION:
APPLICANT: Birkbach, Mark
TITLE OF INVENTION: EPSTEIN BARR VIRUS INDUCED GENES
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacke, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/536,954
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/352,678
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Gates, Edward R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: B0801/7044
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 378 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-536-954-2

Query Match 100.0%; Score 1922; DB 4; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.7e-153;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MDLGRPKMSVLLVALLVIFQVCLCODEVTDDYIGNTTVDYTLFESLCSKKQVRNFKAMF 60
DB 1 MDLGRPKMSVLLVALLVIFQVCLCODEVTDDYIGNTTVDYTLFESLCSKKQVRNFKAMF 60
QY 61 LPIWTSIIICFVGLLNGVLVLTYYIFKRLKTMPTDYLLNLAVADILFLTLTPEFMAVSAK 120
DB 61 LPIWTSIIICFVGLLNGVLVLTYYIFKRLKTMPTDYLLNLAVADILFLTLTPEFMAVSAK 120
QY 121 SWFEGVHFCKLIFAIYKMSFSGMLLLCISIDRYVAIVQAVSARHRRARVLLISKSCV 180
DB 121 SWFEGVHFCKLIFAIYKMSFSGMLLLCISIDRYVAIVQAVSARHRRARVLLISKSCV 180
QY 181 GSAIIATVLSIPELLYSDLRSSSEQARCSLITHEVAFTITIOVAVIGFLVPLAMS 240
DB 181 GSAIIATVLSIPELLYSDLRSSSEQARCSLITHEVAFTITIOVAVIGFLVPLAMS 240
QY 241 FCYLVIRTLQARNPERKAIKVIIAVVVFIVFQLPYNGVLAQTVANFNITSTCEL 300
DB 241 FCYLVIRTLQARNPERKAIKVIIAVVVFIVFQLPYNGVLAQTVANFNITSTCEL 300
QY 301 SKQINIAVDVYSLACVRCVNPFLYAFIGVFRNDIFLFDLGLCSOEOLRQWSSCRH 360
DB 301 SKQINIAVDVYSLACVRCVNPFLYAFIGVFRNDIFLFDLGLCSOEOLRQWSSCRH 360
QY 361 IRRSSMSVBAETTTTFSP 378
DB 361 IRRSSMSVBAETTTTFSP 378
```

RESULT 7

US-09-929-583B-2
Sequence 2, Application US/09929583B
Patent No. 6699971

GENERAL INFORMATION:
APPLICANT: Birkbach, Mark
TITLE OF INVENTION: ANTIBODIES THAT BIND EPSTEIN BARR VIRUS INDUCED PROTEINS
FILE REFERENCE: B0801.70226US00
CURRENT APPLICATION NUMBER: US/09/929,583B
CURRENT FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: US 09/536,954
PRIOR FILING DATE: 2000-03-28
PRIOR APPLICATION NUMBER: US 08/352,678
PRIOR FILING DATE: 1994-11-30
PRIOR APPLICATION NUMBER: US 07/980,518
PRIOR FILING DATE: 1992-11-25
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 378
TYPE: PRT
ORGANISM: Homo sapiens
US-09-929-583B-2

Query Match 100.0%; Score 1922; DB 4; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.7e-153;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MDLGRPKMSVLLVALLVIFQVCLCODEVTDDYIGNTTVDYTLFESLCSKKQVRNFKAMF 60
DB 1 MDLGRPKMSVLLVALLVIFQVCLCODEVTDDYIGNTTVDYTLFESLCSKKQVRNFKAMF 60
QY 61 LPIWTSIIICFVGLLNGVLVLTYYIFKRLKTMPTDYLLNLAVADILFLTLTPEFMAVSAK 120
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Db 61 LPIIMSIICFVGLGGLVLLTYIFKRLKTMTDYLLMLAVADILFLLTLPFWA5AAK 120
Qy 121 SWFGVHFCKLIPAIYKMSFFSGMLLLCISIDRYVAIVQAVSAHRRARVLLISLSCV 180
Db 121 SWFGVHFCKLIPAIYKMSFFSGMLLLCISIDRYVAIVQAVSAHRRARVLLISLSCV 180
Qy 181 GSAILATVLSIBELYSDDLQRSSSEQAMRCSLITEHVEAFITIQVQMWIGFLVPLLA5 240
Db 181 GSAILATVLSIBELYSDDLQRSSSEQAMRCSLITEHVEAFITIQVQMWIGFLVPLLA5 240
Qy 241 FCYLVIRTLQARNERNKAIKVIIVAVVVFIVFQLPYNGVVLAAQTVANFNITSTCEL 300
Db 241 FCYLVIRTLQARNERNKAIKVIIVAVVVFIVFQLPYNGVVLAAQTVANFNITSTCEL 300
Qy 301 SKQMLNAYDVVTSYLACVRCVNPFLYAFYGVKFRNDIFKLFKDLGCLSOBOLRQWSSCRH 360
Db 301 SKQMLNAYDVVTSYLACVRCVNPFLYAFYGVKFRNDIFKLFKDLGCLSOBOLRQWSSCRH 360
Qy 361 IRRSSMSVEAETTTTFFSP 378
Db 361 IRRSSMSVEAETTTTFFSP 378
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```
RESULT 8
US-09-721-341-7
; Sequence 7, Application US/09721341
; Patent No. 6828108
; GENERAL INFORMATION:
; APPLICANT: Goelling, Jennife
; APPLICANT: Dairegh, Daniel J.
; APPLICANT: Hanley, Michael
; APPLICANT: Miao, Zhenhua
; APPLICANT: Schall, Thomas J.
; APPLICANT: ChemoCentryx, Inc.
; TITLE OF INVENTION: Chemokine Receptor
; FILE REFERENCE: 019934-000710US
; CURRENT APPLICATION NUMBER: US/09/721,341
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: US 09/686,020
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/159,015
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: US 60/159,210
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 60/172,979
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 60/173,388
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 60/186,626
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: chemokine receptor (CCR7)
US-09-721-341-7
```

```
Query Match 100.0%; Score 1922; DB 4; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.7e-153;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDLGRKMSVLVVALLVIFQVCLCODEVTDYIGDNTTYDYLPSLCSKQDVNRKAMP 60
Db 1 MDLGRKMSVLVVALLVIFQVCLCODEVTDYIGDNTTYDYLPSLCSKQDVNRKAMP 60
Qy 61 LPIIMSIICFVGLGGLVLLTYIFKRLKTMTDYLLMLAVADILFLLTLPFWA5AAK 120
Db 61 LPIIMSIICFVGLGGLVLLTYIFKRLKTMTDYLLMLAVADILFLLTLPFWA5AAK 120
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Qy 121 SWFGVHFCKLIPAIYKMSFFSGMLLLCISIDRYVAIVQAVSAHRRARVLLISLSCV 180
Db 121 SWFGVHFCKLIPAIYKMSFFSGMLLLCISIDRYVAIVQAVSAHRRARVLLISLSCV 180
Qy 181 GSAILATVLSIBELYSDDLQRSSSEQAMRCSLITEHVEAFITIQVQMWIGFLVPLLA5 240
Db 181 GSAILATVLSIBELYSDDLQRSSSEQAMRCSLITEHVEAFITIQVQMWIGFLVPLLA5 240
Qy 241 FCYLVIRTLQARNERNKAIKVIIVAVVVFIVFQLPYNGVVLAAQTVANFNITSTCEL 300
Db 241 FCYLVIRTLQARNERNKAIKVIIVAVVVFIVFQLPYNGVVLAAQTVANFNITSTCEL 300
Qy 301 SKQMLNAYDVVTSYLACVRCVNPFLYAFYGVKFRNDIFKLFKDLGCLSOBOLRQWSSCRH 360
Db 301 SKQMLNAYDVVTSYLACVRCVNPFLYAFYGVKFRNDIFKLFKDLGCLSOBOLRQWSSCRH 360
Qy 361 IRRSSMSVEAETTTTFFSP 378
Db 361 IRRSSMSVEAETTTTFFSP 378
```

```
RESULT 9
US-09-721-495B-7
; Sequence 7, Application US/09721495B
; Patent No. 683547
; GENERAL INFORMATION:
; APPLICANT: Goelling, Jennife
; APPLICANT: Dairegh, Daniel J.
; APPLICANT: Hanley, Michael
; APPLICANT: Miao, Zhenhua
; APPLICANT: Talbot, Dale
; APPLICANT: Schall, Thomas J.
; APPLICANT: ChemoCentryx, Inc.
; TITLE OF INVENTION: Chemokine Receptor
; FILE REFERENCE: 019934-0007210US
; CURRENT APPLICATION NUMBER: US/09/721,495B
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: US 60/159,015
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: US 60/159,210
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 60/172,979
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 60/173,388
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 60/186,626
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: US 09/686,019
; PRIOR FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: chemokine receptor CCR7
US-09-721-495B-7
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```
Query Match 100.0%; Score 1922; DB 4; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.7e-153;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDLGRKMSVLVVALLVIFQVCLCODEVTDYIGDNTTYDYLPSLCSKQDVNRKAMP 60
Db 1 MDLGRKMSVLVVALLVIFQVCLCODEVTDYIGDNTTYDYLPSLCSKQDVNRKAMP 60
Qy 61 LPIIMSIICFVGLGGLVLLTYIFKRLKTMTDYLLMLAVADILFLLTLPFWA5AAK 120
Db 61 LPIIMSIICFVGLGGLVLLTYIFKRLKTMTDYLLMLAVADILFLLTLPFWA5AAK 120
Qy 121 SWFGVHFCKLIPAIYKMSFFSGMLLLCISIDRYVAIVQAVSAHRRARVLLISLSCV 180
Db 121 SWFGVHFCKLIPAIYKMSFFSGMLLLCISIDRYVAIVQAVSAHRRARVLLISLSCV 180
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Db 121 SWFGVHCKLIFAIYKMSFSGMLLLCISIDRYVAIVQAVSARHRAVLLISKSCV 180
QY 181 GSALATATVLSIPBELLYSDLQRSSSSQAMRCSLITEHVEAFITIOVAQWVIGLVPPLAMS 240
Db 181 GSALATATVLSIPBELLYSDLQRSSSSQAMRCSLITEHVEAFITIOVAQWVIGLVPPLAMS 240
QY 241 FCYLVITITLLQARNPERKAIKVIIAVVVFIVFQLPYNGVLAQTVANFNITSTCEL 300
Db 241 FCYLVITITLLQARNPERKAIKVIIAVVVFIVFQLPYNGVLAQTVANFNITSTCEL 300
QY 301 SKQNIADVTYSLACVRCNPFYAFIGVFRNDIFKLFDJGCLSQEQLRQWSSCRH 360
Db 301 SKQNIADVTYSLACVRCNPFYAFIGVFRNDIFKLFDJGCLSQEQLRQWSSCRH 360
QY 361 IRRSSMSVEAETTTTFFSP 378
Db 361 IRRSSMSVEAETTTTFFSP 378

RESULT 10

PCT-US93-09636-2
; Sequence 2, Application PC/TUS9309636
; GENERAL INFORMATION:
; APPLICANT: Birkenbach, Mark
; TITLE OF INVENTION: Epstein Barr Virus Induced Genes
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/09636
; FILING DATE: herewith
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; PCT-US93-09636-2

Query Match 100.0%; Score 1922; DB 5; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.7e-153;

Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MDLGRKMSVVLVALLVIFQVCLCODEVTDDYIGNTTVDYTLFESLCSKQDVRFKAMF 60
QY 61 LPIMYSIICFVGLNGVLVLTYYIFKRLKTMTDYLLNLAVADILFLTLTLPFMAVSAK 120
Db 61 LPIMYSIICFVGLNGVLVLTYYIFKRLKTMTDYLLNLAVADILFLTLTLPFMAVSAK 120
QY 121 SWFGVHCKLIFAIYKMSFSGMLLLCISIDRYVAIVQAVSARHRAVLLISKSCV 180
Db 121 SWFGVHCKLIFAIYKMSFSGMLLLCISIDRYVAIVQAVSARHRAVLLISKSCV 180
QY 181 GSALATATVLSIPBELLYSDLQRSSSSQAMRCSLITEHVEAFITIOVAQWVIGLVPPLAMS 240
Db 181 GSALATATVLSIPBELLYSDLQRSSSSQAMRCSLITEHVEAFITIOVAQWVIGLVPPLAMS 240

QY 241 FCYLVITITLLQARNPERKAIKVIIAVVVFIVFQLPYNGVLAQTVANFNITSTCEL 300
Db 241 FCYLVITITLLQARNPERKAIKVIIAVVVFIVFQLPYNGVLAQTVANFNITSTCEL 300
QY 301 SKQNIADVTYSLACVRCNPFYAFIGVFRNDIFKLFDJGCLSQEQLRQWSSCRH 360
Db 301 SKQNIADVTYSLACVRCNPFYAFIGVFRNDIFKLFDJGCLSQEQLRQWSSCRH 360
QY 361 IRRSSMSVEAETTTTFFSP 378
Db 361 IRRSSMSVEAETTTTFFSP 378

RESULT 11

US-08-153-848-15
; Sequence 15, Application US/08153848
; Patent No. 5759804
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 5759804e1 Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/153,848
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5759804and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-153-848-15

Query Match 99.2%; Score 1907; DB 1; Length 378;
Best Local Similarity 99.2%; Pred. No. 3.1e-152;

Matches 375; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDLGRKMSVVLVALLVIFQVCLCODEVTDDYIGNTTVDYTLFESLCSKQDVRFKAMF 60
Db 1 MDLGRKMSVVLVALLVIFQVCLCODEVTDDYIGNTTVDYTLFESLCSKQDVRFKAMF 60
QY 61 LPIMYSIICFVGLNGVLVLTYYIFKRLKTMTDYLLNLAVADILFLTLTLPFMAVSAK 120
Db 61 LPIMYSIICFVGLNGVLVLTYYIFKRLKTMTDYLLNLAVADILFLTLTLPFMAVSAK 120
QY 121 SWFGVHCKLIFAIYKMSFSGMLLLCISIDRYVAIVQAVSARHRAVLLISKSCV 180
Db 121 SWFGVHCKLIFAIYKMSFSGMLLLCISIDRYVAIVQAVSARHRAVLLISKSCV 180

Db 121 SWFGVHPCKLFAIYKMSFSGMLLLCLSIDRYVAIVQASAHRRARVLLISKSCV 180
QY 181 GSAIATVLSIPBELYSDIQRSSSEQAMRCSLITHEVEAFITIQVQMWIGFLVPLIAMS 240
Db 181 GIMILATVLSIPBELYSDIQRSSSEQAMRCSLITHEVEAFITIQVQMWIGFLVPLIAMS 240
QY 241 FCYLVIIIRTLQARNFERNKAIKVIIVVVFIVFQLPYNGVLAQTVANFNITSTCEL 300
Db 241 FCYLVIIIRTLQARNFERNKAIKVIIVVVFIVFQLPYNGVLAQTVANFNITSTCEL 300
QY 301 SKQNLNAVDTYSLACVRCNPNFLYAFIGVFRNDIFKLPKDLGCLSGOQLRQWSSCRH 360
Db 301 SKQNLNAVDTYSLACVRCNPNFLYAFIGVFRNDIFKLPKDLGCLSGOQLRQWSSCRH 360
QY 361 IRRSSMSVEAETTTTSP 378
Db 361 IRRSSMSVEAETTTTSP 378

RESULT 12
US-09-299-843A-15
Sequence 15, Application US/09299843A
Patent No. 6107475
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schwellhart, Vicki L.
TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,843A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Jili E. Uhl
REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/32059B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-299-843A-15

Query Match 99.2%; Score 1907; DB 3; Length 378;
Best Local Similarity 99.2%; Pred. No. 3,le-152;

Matches 375; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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Db 1 MDGKPMKSVLVALLVIFQVCLCODEVTDDYIGDNTVDTYTLFESLCSKRDVRFKAMF 60
QY 61 LPIWYSIICFVGILGNGLVLTYYIKRLKTMDDTYLLNLAVADILFLTLPMWASAAK 120
Db 61 LPIWYSIICFVGILGNGLVLTYYIKRLKTMDDTYLLNLAVADILFLTLPMWASAAK 120
QY 121 SWFGVHPCKLFAIYKMSFSGMLLLCLSIDRYVAIVQASAHRRARVLLISKSCV 180
Db 121 SWFGVHPCKLFAIYKMSFSGMLLLCLSIDRYVAIVQASAHRRARVLLISKSCV 180
QY 181 GSAIATVLSIPBELYSDIQRSSSEQAMRCSLITHEVEAFITIQVQMWIGFLVPLIAMS 240
Db 181 GIMILATVLSIPBELYSDIQRSSSEQAMRCSLITHEVEAFITIQVQMWIGFLVPLIAMS 240
QY 241 FCYLVIIIRTLQARNFERNKAIKVIIVVVFIVFQLPYNGVLAQTVANFNITSTCEL 300
Db 241 FCYLVIIIRTLQARNFERNKAIKVIIVVVFIVFQLPYNGVLAQTVANFNITSTCEL 300
QY 301 SKQNLNAVDTYSLACVRCNPNFLYAFIGVFRNDIFKLPKDLGCLSGOQLRQWSSCRH 360
Db 301 SKQNLNAVDTYSLACVRCNPNFLYAFIGVFRNDIFKLPKDLGCLSGOQLRQWSSCRH 360
QY 361 IRRSSMSVEAETTTTSP 378
Db 361 IRRSSMSVEAETTTTSP 378

RESULT 13
US-09-251-545-1
Sequence 1, Application US/09251545
Patent No. 6153441
GENERAL INFORMATION:
APPLICANT: Edward R. Appelbaum
APPLICANT: Henry M. Sarau
APPLICANT: John R. White
TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND
TITLE OF INVENTION: ANTAGONISTS OF THE INTERACTION BETWEEN HUMAN CCR7 RECEPTOR
AND CCR9 LIGAND AND INTERACTION THEREOF
FILE REFERENCE: P50753
CURRENT FILING DATE: 1999-02-17
EARLIER APPLICATION NUMBER: US/09/251,545
EARLIER FILING DATE: 1998-02-17
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for windows Version 3.0
SEQ ID NO 1
LENGTH: 378
TYPE: PRT
ORGANISM: Human
US-09-251-545-1

Query Match 99.2%; Score 1907; DB 3; Length 378;
Best Local Similarity 99.2%; Pred. No. 3,le-152;
Matches 375; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MDGKPMKSVLVALLVIFQVCLCODEVTDDYIGDNTVDTYTLFESLCSKRDVRFKAMF 60
Db 1 MDGKPMKSVLVALLVIFQVCLCODEVTDDYIGDNTVDTYTLFESLCSKRDVRFKAMF 60
QY 61 LPIWYSIICFVGILGNGLVLTYYIKRLKTMDDTYLLNLAVADILFLTLPMWASAAK 120
Db 61 LPIWYSIICFVGILGNGLVLTYYIKRLKTMDDTYLLNLAVADILFLTLPMWASAAK 120
QY 121 SWFGVHPCKLFAIYKMSFSGMLLLCLSIDRYVAIVQASAHRRARVLLISKSCV 180
Db 121 SWFGVHPCKLFAIYKMSFSGMLLLCLSIDRYVAIVQASAHRRARVLLISKSCV 180
QY 181 GSAIATVLSIPBELYSDIQRSSSEQAMRCSLITHEVEAFITIQVQMWIGFLVPLIAMS 240
Db 181 GIMILATVLSIPBELYSDIQRSSSEQAMRCSLITHEVEAFITIQVQMWIGFLVPLIAMS 240

Db 181 GIMILATVLSIPELLYSDLQRRSSSQAMRCSLITEHVEAFITIQVAQWVIGFLVPLLAMS 240
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Db 241 FCYLVITRTLOARPERKKAIVIIAVVVVFIQVLPYNGVLAQTVANFNITSTCEL 300
Qy 301 SKQNLIAVDVYSLACVRCVNPFLYAFIGVFRNDIFKLFDLGLCLSGEQLRQWSSCGH 360
Db 301 SKQNLIAVDVYSLACVRCVNPFLYAFIGVFRNDIFKLFDLGLCLSGEQLRQWSSCGH 360
Qy 361 IRRSSMSVEAETTTTTFSP 378
Db 361 IRRSSMSVEAETTTTTFSP 378

RESULT 14
US-09-088-337B-15
; Sequence 15, Application US/09088337B
; Patent No. 6348574
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; Gray, Patrick W.
; Schmelkart, Vicki L.
; TITLE OF INVENTION: No. 6348574e1 Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Marshall, O'Toole, Gerstein, Murray &
; Borum
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Releasee #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/088,337B
; FILING DATE: 01-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6348574and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-088-337B-15

Query Match 99.2%; Score 1907; DB 3; Length 378;
Best Local Similarity 99.2%; Pred. No. 3.1e-152;
Matches 375; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MDLGRKMSVLLVALLVIFQVCLCODEVTDDYIGDNTTVDYTLFBSLCSKKDVRNFKAF 60
Db 1 MDLGRKMSVLLVALLVIFQVCLCODEVTDDYIGDNTTVDYTLFBSLCSKKDVRNFKAF 60
Qy 61 LPIMYSIIICFVGLDNGVLLVLYIFKRLKMTDITYLLNLAAVADILFLTLTFFMAYSAK 120
Db 61 LPIMYSIIICFVGLDNGVLLVLYIFKRLKMTDITYLLNLAAVADILFLTLTFFMAYSAK 120

Db 61 LPIMYSIIICFVGLDNGVLLVLYIFKRLKMTDITYLLNLAAVADILFLTLTFFMAYSAK 120
Qy 121 SWVFGVHCKLIIFAIYKNSPFGMLLLCISIDRYVAIVQAVSAHRHARVLLISKLSGV 180
Db 121 SWVFGVHCKLIIFAIYKNSPFGMLLLCISIDRYVAIVQAVSAHRHARVLLISKLSGV 180
Qy 181 GSAILIATVLSIPELLYSDLQRRSSSQAMRCSLITEHVEAFITIQVAQWVIGFLVPLLAMS 240
Db 181 GSAILIATVLSIPELLYSDLQRRSSSQAMRCSLITEHVEAFITIQVAQWVIGFLVPLLAMS 240
Qy 241 FCYLVITRTLOARPERKKAIVIIAVVVVFIQVLPYNGVLAQTVANFNITSTCEL 300
Db 241 FCYLVITRTLOARPERKKAIVIIAVVVVFIQVLPYNGVLAQTVANFNITSTCEL 300
Qy 301 SKQNLIAVDVYSLACVRCVNPFLYAFIGVFRNDIFKLFDLGLCLSGEQLRQWSSCGH 360
Db 301 SKQNLIAVDVYSLACVRCVNPFLYAFIGVFRNDIFKLFDLGLCLSGEQLRQWSSCGH 360
Qy 361 IRRSSMSVEAETTTTTFSP 378
Db 361 IRRSSMSVEAETTTTTFSP 378

RESULT 15
US-09-170-496D-74
; Sequence 74, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-(
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 74
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-170-496D-74

Query Match 99.2%; Score 1907; DB 4; Length 378;
Best Local Similarity 99.2%; Pred. No. 3.1e-152;
Matches 375; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Db 1 MDLGRKMSVLLVALLVIFQVCLCODEVTDDYIGDNTTVDYTLFBSLCSKKDVRNFKAF 60
Qy 61 LPIMYSIIICFVGLDNGVLLVLYIFKRLKMTDITYLLNLAAVADILFLTLTFFMAYSAK 120
Db 61 LPIMYSIIICFVGLDNGVLLVLYIFKRLKMTDITYLLNLAAVADILFLTLTFFMAYSAK 120
Qy 121 SWVFGVHCKLIIFAIYKNSPFGMLLLCISIDRYVAIVQAVSAHRHARVLLISKLSGV 180
Db 121 SWVFGVHCKLIIFAIYKNSPFGMLLLCISIDRYVAIVQAVSAHRHARVLLISKLSGV 180
Qy 181 GSAILIATVLSIPELLYSDLQRRSSSQAMRCSLITEHVEAFITIQVAQWVIGFLVPLLAMS 240
Db 181 GSAILIATVLSIPELLYSDLQRRSSSQAMRCSLITEHVEAFITIQVAQWVIGFLVPLLAMS 240
Qy 241 FCYLVITRTLOARPERKKAIVIIAVVVVFIQVLPYNGVLAQTVANFNITSTCEL 300
Db 241 FCYLVITRTLOARPERKKAIVIIAVVVVFIQVLPYNGVLAQTVANFNITSTCEL 300
Qy 301 SKQNLIAVDVYSLACVRCVNPFLYAFIGVFRNDIFKLFDLGLCLSGEQLRQWSSCGH 360
Db 301 SKQNLIAVDVYSLACVRCVNPFLYAFIGVFRNDIFKLFDLGLCLSGEQLRQWSSCGH 360

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Db	361	IRSSMSVEAETTTTSP	378

Search completed: February 25, 2005, 02:24:33
Job time : 45 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: February 25, 2005, 02:23:03 ; Search time 134 Seconds
(without alignments)
923.113 Million cell updates/sec

Title: US-10-749-990-2

Perfect score: 1922
Sequence: 1 MDLGRPKMSVLLVALLVIFQ.....RHRRSSMSVEAETTTTSP 378

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1380268 seqs, 327241040 residues

Total number of hits satisfying chosen parameters: 1380268

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA.*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1922	100.0	378	9	US-09-929-583B-2
2	1922	100.0	378	14	US-10-164-649-49
3	1922	100.0	378	16	US-10-749-990-2
4	1907	99.2	378	14	US-10-251-385-74
5	1907	99.2	378	14	US-10-225-567A-68
6	1907	99.2	378	14	US-10-239-423-70
7	1907	99.2	378	15	US-10-435-696-48
8	1900	98.9	378	14	US-10-251-385-204
9	1814	94.4	475	15	US-10-425-114-56811
10	758.5	39.5	357	9	US-09-903-377-2
11	758.5	39.5	357	9	US-09-952-385-2
12	758.5	39.5	357	10	US-09-966-755-2
13	758.5	39.5	357	13	US-10-000-759A-2

14	758.5	39.5	357	14	US-10-251-385-24	Sequence 24, Appl
15	758.5	39.5	357	14	US-10-225-567A-241	Sequence 241, App
16	758.5	39.5	357	14	US-10-239-423-73	Sequence 73, Appl
17	758.5	39.5	357	14	US-10-239-423-72	Sequence 72, Appl
18	753.5	39.2	357	14	US-10-251-385-176	Sequence 176, Appl
19	753.5	39.2	357	10	US-09-825-509-481	Sequence 481, App
20	753.5	39.2	357	17	US-10-925-095-481	Sequence 481, App
21	707.5	36.8	369	14	US-10-239-423-69	Sequence 69, Appl
22	707.5	36.8	374	14	US-10-164-649-48	Sequence 48, Appl
23	707.5	36.8	374	14	US-10-239-423-68	Sequence 68, Appl
24	707.5	36.8	390	13	US-10-087-192-1920	Sequence 1920, Ap
25	707.5	36.8	406	14	US-10-325-430-18	Sequence 18, Appl
26	707.5	36.8	406	14	US-10-025-386-32911	Sequence 32911, A
27	704.5	36.7	374	14	US-10-225-567A-390	Sequence 390, App
28	703	36.6	367	14	US-10-254-089-2	Sequence 2, Appl1
29	703	36.6	367	13	US-10-244-089-2	Sequence 2, Appl1
30	703	36.6	408	15	US-10-087-192-1917	Sequence 1917, Ap
31	664	34.5	365	15	US-10-643-431-8	Sequence 8, Appl1
32	663	34.5	365	14	US-10-039-659-10	Sequence 10, Appl
33	663	34.5	365	16	US-10-754-071-10	Sequence 10, Appl
34	650	33.8	350	10	US-09-910-695-8	Sequence 8, Appl1
35	643	33.5	350	9	US-09-765-994-2	Sequence 2, Appl1
36	643	33.5	350	9	US-09-796-338A-8	Sequence 8, Appl1
37	643	33.5	350	10	US-09-966-433-16	Sequence 16, Appl
38	643	33.5	350	14	US-10-282-837-8	Sequence 8, Appl1
39	643	33.5	350	14	US-10-225-567A-607	Sequence 607, App
40	643	33.5	350	14	US-10-288-222A-10	Sequence 10, Appl
41	643	33.5	350	14	US-10-145-586-8	Sequence 8, Appl1
42	643	33.5	350	14	US-10-239-423-75	Sequence 75, Appl
43	643	33.5	350	15	US-10-407-079-84	Sequence 84, Appl
44	642	33.4	348	15	US-10-403-161-12	Sequence 12, Appl
45	642	33.4	349	9	US-09-765-994-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1
US-09-929-583B-2
; Sequence 2, Application US/09929583B
; Publication No. US20020040133A1
; GENERAL INFORMATION:
; APPLICANT: Birkendach, Mark
; APPLICANT: Kieff, Elliot
; TITLE OF INVENTION: ANTIBODIES THAT BIND EBSTEIN BARR VIRUS INDUCED PROTEINS
; FILE REFERENCE: B0801.70226US00
; CURRENT APPLICATION NUMBER: US/09/929,583B
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 09/536,954
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: US 08/352,678
; PRIOR FILING DATE: 1994-11-30
; PRIOR APPLICATION NUMBER: US 07/980,518
; PRIOR FILING DATE: 1992-11-25
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-929-583B-2
Query Match 100.0%; Score 1922; DB 9; Length 378;
Best Local Similarity 100.0%; Pred. No. 2,3e-158; Mismatches 0; Indels 0; Gaps 0;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDLGRPKMSVLLVALLVIFQVCLCODEVTDDYIGNTTVDYTLFSLCSKKQVRNFKAF 60
DB 1 MDLGRPKMSVLLVALLVIFQVCLCODEVTDDYIGNTTVDYTLFSLCSKKQVRNFKAF 60
QY 61 LPIMSIICFVGLLNGGLVLTYYIFPKRLKMTDTYLLNLAVADILFLTLTFFMAYSAK 120
DB 61 LPIMSIICFVGLLNGGLVLTYYIFPKRLKMTDTYLLNLAVADILFLTLTFFMAYSAK 120

QY 121 SWFGVHFCCKLIPAIYKMSFSGMILLICISIDRYVAIVQAVSARHRRARVLLISKLSCV 180
DB 121 SWFGVHFCCKLIPAIYKMSFSGMILLICISIDRYVAIVQAVSARHRRARVLLISKLSCV 180
QY 181 GSAILATVLSIPPELLYSDLQRRSSSEQAMRCSLITEHVEAFITTIQVAQWVIGFLVPLLAMS 240
DB 181 GSAILATVLSIPPELLYSDLQRRSSSEQAMRCSLITEHVEAFITTIQVAQWVIGFLVPLLAMS 240
QY 241 FCYLVITIRTLQARNFERNKAIKVIIAVVVVFIQOLPYNGVLAQTVANFNITSTCEL 300
DB 241 FCYLVITIRTLQARNFERNKAIKVIIAVVVVFIQOLPYNGVLAQTVANFNITSTCEL 300
QY 301 SKQINIAVDVYSLACVRCNPFYAFIYKFRNDIFKLFDGLGCLSOEOLRQMSCCR 360
DB 301 SKQINIAVDVYSLACVRCNPFYAFIYKFRNDIFKLFDGLGCLSOEOLRQMSCCR 360
QY 361 IRRSSMSVEAETTTTFSP 378
DB 361 IRRSSMSVEAETTTTFSP 378

RESULT 2

US-10-164-649-49
; Sequence 49, Application US/10164649
; Publication No. US20030162943A1
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. US20030162943A1 Molecules of the G Protein-Coupled
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSER: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/164,649
; FILING DATE: 07-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/045,583
; FILING DATE: 20-MAR-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-10-164-649-49

Query Match 100.0%; Score 1922; DB 14; Length 378;
Best Local Similarity 100.0%; Pred.No. 2.3e-158; Indels 0; Gaps 0;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLGRKMSVLLVALLVIFQVCLCODEVTDYIGNTTVDYTLFESLSCKDVRNFKAMF 60
DB 1 MDLGRKMSVLLVALLVIFQVCLCODEVTDYIGNTTVDYTLFESLSCKDVRNFKAMF 60

QY 61 LPIMYSIIICFVGLGNGLVLTYYIFKRLKMTDTYILNLAVADTLFLLTLPFMAYSAAK 120
DB 61 LPIMYSIIICFVGLGNGLVLTYYIFKRLKMTDTYILNLAVADTLFLLTLPFMAYSAAK 120
QY 121 SWFGVHFCCKLIPAIYKMSFSGMILLICISIDRYVAIVQAVSARHRRARVLLISKLSCV 180
DB 121 SWFGVHFCCKLIPAIYKMSFSGMILLICISIDRYVAIVQAVSARHRRARVLLISKLSCV 180
QY 181 GSAILATVLSIPPELLYSDLQRRSSSEQAMRCSLITEHVEAFITTIQVAQWVIGFLVPLLAMS 240
DB 181 GSAILATVLSIPPELLYSDLQRRSSSEQAMRCSLITEHVEAFITTIQVAQWVIGFLVPLLAMS 240
QY 241 FCYLVITIRTLQARNFERNKAIKVIIAVVVVFIQOLPYNGVLAQTVANFNITSTCEL 300
DB 241 FCYLVITIRTLQARNFERNKAIKVIIAVVVVFIQOLPYNGVLAQTVANFNITSTCEL 300
QY 301 SKQINIAVDVYSLACVRCNPFYAFIYKFRNDIFKLFDGLGCLSOEOLRQMSCCR 360
DB 301 SKQINIAVDVYSLACVRCNPFYAFIYKFRNDIFKLFDGLGCLSOEOLRQMSCCR 360
QY 361 IRRSSMSVEAETTTTFSP 378
DB 361 IRRSSMSVEAETTTTFSP 378

RESULT 3

US-10-749-990-2
; Sequence 2, Application US/10749990
; Publication No. US20040138418A1
; GENERAL INFORMATION:
; APPLICANT: Birkenbach, Mark
; APPLICANT: Kieft, Elliot
; TITLE OF INVENTION: EPSTEIN BARR VIRUS INDUCED GENES
; FILE REFERENCE: B0801.70226US01
; CURRENT APPLICATION NUMBER: US/10/749,990
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 09/929,583
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 09/536,954
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: US 08/352,678
; PRIOR FILING DATE: 1994-11-30
; PRIOR APPLICATION NUMBER: US 07/980,518
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-749-990-2

Query Match 100.0%; Score 1922; DB 16; Length 378;
Best Local Similarity 100.0%; Pred.No. 2.3e-158; Indels 0; Gaps 0;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLGRKMSVLLVALLVIFQVCLCODEVTDYIGNTTVDYTLFESLSCKDVRNFKAMF 60
DB 1 MDLGRKMSVLLVALLVIFQVCLCODEVTDYIGNTTVDYTLFESLSCKDVRNFKAMF 60
QY 61 LPIMYSIIICFVGLGNGLVLTYYIFKRLKMTDTYILNLAVADTLFLLTLPFMAYSAAK 120
DB 61 LPIMYSIIICFVGLGNGLVLTYYIFKRLKMTDTYILNLAVADTLFLLTLPFMAYSAAK 120
QY 121 SWFGVHFCCKLIPAIYKMSFSGMILLICISIDRYVAIVQAVSARHRRARVLLISKLSCV 180
DB 121 SWFGVHFCCKLIPAIYKMSFSGMILLICISIDRYVAIVQAVSARHRRARVLLISKLSCV 180
QY 181 GSAILATVLSIPPELLYSDLQRRSSSEQAMRCSLITEHVEAFITTIQVAQWVIGFLVPLLAMS 240
DB 181 GSAILATVLSIPPELLYSDLQRRSSSEQAMRCSLITEHVEAFITTIQVAQWVIGFLVPLLAMS 240

Qy	241	FCYVIVIRTLQANFEENKAIKVIIAVWVFIVQLPNGVLAQTANFNITSTCEL	300
Dd	241	FCYVIVIRTLQANFEENKAIKVIIAVWVFIVQLPNGVLAQTANFNITSTCEL	300
Qy	301	SKQINIAVDVTYSIACVRCVCVPFLYAFIGVKFRNDIFCLFDGLCSOQLROMSSCRH	360
Dd	301	SKQINIAVDVTYSIACVRCVCVPFLYAFIGVKFRNDIFCLFDGLCSOQLROMSSCRH	360
Qy	361	IRRSMSVEAETTTTFFSP	378
Dd	361	IRRSMSVEAETTTTFFSP	378

```

RESULT 4
US-10-251-385-74
; Sequence 74, Application US/10251385
; Publication No. US20030105292A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; TITLE OF INVENTION: Lisw, Chen W.
; TITLE OF INVENTION: No. US20030105292A1-Endogenous, Constitutively Activated Human G
; TITLE OF INVENTION: Protein-Coupled
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/10/251,385
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 74
; LENGTH: 378
; TYPE: prt
; ORGANISM: Homo sapiens
; US-10-251-385-74

```

Query Match	99.2%	Score 1907	DB 14	Length 378
Beat Local Similarity	99.2%	Pred. No. 4	6e-157	
Matches 375	Conservative 1	Mismatches 2	Indels 0	Gaps 0
QY	1	MDLCKPMKSVLVALVLLVIFQVCLCODEVTDYDIGNTVTVDYTLFESLCSKKDVRNFKAMF	60	
Db	1	MDLCKPMKSVLVALVLLVIFQVCLCODEVTDYDIGNTVTVDYTLFESLCSKKDVRNFKAMF	60	
QY	61	LPIMYSIIICFGLGNGLVLTLYIKPKLKTMDTVYLNTAAVDLIFLTLTFPMAYSAK	120	
Db	61	LPIMYSIIICFGLGNGLVLTLYIKPKLKTMDTVYLNTAAVDLIFLTLTFPMAYSAK	120	
QY	121	SWEGVHFCKLIFAIYKMSFESGMILLICISIDRVVAIQVAASARHRRARVLLISLSCV	180	
Db	121	SWEGVHFCKLIFAIYKMSFESGMILLICISIDRVVAIQVAASARHRRARVLLISLSCV	180	
QY	181	GSALLATVLTSLPELLYSDLORSSSEQARCSLITHEVEAFITIQVAQWYIGLVPLILMS	240	
Db	181	GIWLATVLTSLPELLYSDLORSSSEQARCSLITHEVEAFITIQVAQWYIGLVPLILMS	240	
QY	241	FCYLVIIITKLQARNFERNKAIKVITIAVVVVEIVQLPNGVVLQCTVANFNITSCTEL	300	
Db	241	FCYLVIIITKLQARNFERNKAIKVITIAVVVVEIVQLPNGVVLQCTVANFNITSCTEL	300	
QY	301	SKOLNIADVTVYSLACVRCVNPFLYAFIGVFRNDIFKLFDQLCLSGEQLRQWSSCH	360	
Db	301	SKOLNIADVTVYSLACVRCVNPFLYAFIGVFRNDIFKLFDQLCLSGEQLRQWSSCH	360	
QY	361	IRRSMSVEAETTTTFFSP	378	
Db	361	IRRSMSVEAETTTTFFSP	378	

RESULT 5
US-10-225-567A-68
; Sequence 68, Application US/10225567A

```

: Publication No. US20030113798A1
: GENERAL INFORMATION:
: APPLICANT: Lifespan Biosciences
: APPLICANT: Brown, Joseph P.
: APPLICANT: Burner, Glenna C.
: APPLICANT: Roush, Christine L.
: TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
: FILE REFERENCE: 1920-4-4
: CURRENT APPLICATION NUMBER: US/10/225,567A
: CURRENT FILING DATE: 2001-12-19
: PRIOR APPLICATION NUMBER: 60/257,144
: PRIOR FILING DATE: 2000-12-19
: NUMBER OF SEQ ID NOS: 2292
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 68
: LENGTH: 378
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-225-567A-68

Query Match          99.2%; Score 1907; DB 14; Length 378;
Best Local Similarity 99.2%; Pred. No. 4 6e-157;
Matches 375; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY	1	MDJGKPKMSLVALLAVI	FOVCLCODEVTDYD	IGDNTVDDYTL	FESLCSKQDVRNKRAMP	60
Db	1	MDJGKPKMSLVALLAVI	FOVCLCODEVTDYD	IGDNTVDDYTL	FESLCSKQDVRNKRAMP	60
QY	61	LPIMYSIICFVGLNGVL	VLYIYFRKLKTM	DTYLLNLAVADII	FLTLTPFWAYSAAK	120
Db	61	LPIMYSIICFVGLNGVL	VLYIYFRKLKTM	DTYLLNLAVADII	FLTLTPFWAYSAAK	120
QY	121	SWFPGVHFCULI	PAIYKMSFPGMLLL	CLSIDRYAIVQAVSAH	HRBPAVLLISLSCV	180
Db	121	SWFPGVHFCULI	PAIYKMSFPGMLLL	CLSIDRYAIVQAVSAH	HRBPAVLLISLSCV	180
QY	181	GSAILNTVLSI	PELTVSDLORSSSE	QAMRCSLITTEHVEAF	ITTVQAVQMWIGFVPLILAMS	240
Db	181	GSAILNTVLSI	PELTVSDLORSSSE	QAMRCSLITTEHVEAF	ITTVQAVQMWIGFVPLILAMS	240
QY	241	FCYLVIIIRTLQARN	FERNKAIKVIIIAV	VVVFIVFOLPYNGV	LAOTVANFNITSSITCEL	300
Db	241	FCYLVIIIRTLQARN	FERNKAIKVIIIAV	VVVFIVFOLPYNGV	LAOTVANFNITSSITCEL	300
QY	301	SKQLNIAVDYTVSL	ACRCQVNPFLYAF	IGVKRRNDIFKL	FKDLGCLSQQLQWSSCRH	360
Db	301	SKQLNIAVDYTVSL	ACRCQVNPFLYAF	IGVKRRNDIFKL	FKDLGCLSQQLQWSSCRH	360
QY	361	IRRSSMSVEAETTTT	FSP	378		
Db	361	IRRSSMSVEAETTTT	FSP	378		

```

RESULT 6
US-10-239-423-70
: Sequence 70, Application US/10239423
: Publication No. US20030186889A1
GENERAL INFORMATION:
APPLICANT: FORSSMANN, Wolf-Georg; FORSSMANN, Ulf; ABERMANN, Knut;
APPLICANT: HEITLAND, Alexandra; SPODSBERG, Nikolaj
TITLE OF INVENTION: Diagnostic Agent and Medicament for Examining the
TITLE OF INVENTION: Cell Surface Proteome of Tumor and Inflammation Cells and
TITLE OF INVENTION: for Treating Tumor Diseases and Inflammatory Diseases,
TITLE OF INVENTION: Preferably with the Aid of Specific Chemokine
TITLE OF INVENTION: Receptor Analytels and Chemokine Receptor/Ligand Interaction
FILE REFERENCE: 022217us
CURRENT APPLICATION NUMBER: US/10/239,423
CURRENT FILING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: DE10016013.1
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 84
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 70

```

LENGTH: 378
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Amino Acid Sequence for the Generation of Antibodies
US-10-239-423-70

Query Match 99.2%; Score 1907; DB 14; Length 378;
Best Local Similarity 99.2%; Pred. No. 4,6e-157;
Matches 375; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDLGRPKMSVLLVALLVIFQVCLCODEVTDYIGNTTVDYTLFESLSCKDVRNFKAMF 60
DB 1 MDLGRPKMSVLLVALLVIFQVCLCODEVTDYIGNTTVDYTLFESLSCKDVRNFKAMF 60
QY 61 LPIWTSIIICFVGLGNGVLVLTYYIFKRLKMTDLYLNLAVADILFLTLTLPFMAYSAAK 120
DB 61 LPIWTSIIICFVGLGNGVLVLTYYIFKRLKMTDLYLNLAVADILFLTLTLPFMAYSAAK 120
QY 121 SWPFGVHFCKLIIFAIYKMSFSGMILLICISIDRYVAIVQAVSAHRHARVLLISKLSCV 180
DB 121 SWPFGVHFCKLIIFAIYKMSFSGMILLICISIDRYVAIVQAVSAHRHARVLLISKLSCV 180
QY 121 SWPFGVHFCKLIIFAIYKMSFSGMILLICISIDRYVAIVQAVSAHRHARVLLISKLSCV 180
DB 121 SWPFGVHFCKLIIFAIYKMSFSGMILLICISIDRYVAIVQAVSAHRHARVLLISKLSCV 180
QY 161 GSAILATVLSIPBELYSDLRSSSSQAMRCSLITEHVEAFITIOVAQWVIGFLVPLAMS 240
DB 161 GSAILATVLSIPBELYSDLRSSSSQAMRCSLITEHVEAFITIOVAQWVIGFLVPLAMS 240
QY 241 FCYLVIIITLLQARNFERKAKVILIAVVVFIYVQLPYNGVLAQTVANFNITSTCEL 300
DB 241 FCYLVIIITLLQARNFERKAKVILIAVVVFIYVQLPYNGVLAQTVANFNITSTCEL 300
QY 301 SKQNLIAVDVYSLACVRCNPFYAFIYKFRNDIFKLFQDLGCLSGEQLRQWSSCRH 360
DB 301 SKQNLIAVDVYSLACVRCNPFYAFIYKFRNDIFKLFQDLGCLSGEQLRQWSSCRH 360
QY 361 IRRSSMSVEAETTTTFSP 378
DB 361 IRRSSMSVEAETTTTFSP 378

RESULT 7

US-10-435-696-48
Sequence 48, Application US/10435696
Publication No. US20040018525A1
GENERAL INFORMATION:
APPLICANT: Munitz, Ralph
APPLICANT: Munitz, Marc
APPLICANT: Kallabis, Harald
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE PREDICTION, DIAGNOSIS, PROGNOSIS
FILE REFERENCE: lea 36 108
CURRENT APPLICATION NUMBER: US/10/435,696
CURRENT FILING DATE: 2003-05-09
PRIOR APPLICATION NUMBER: EP03003112.4
PRIOR FILING DATE: 2003-02-13
PRIOR APPLICATION NUMBER: EP02010291.9
PRIOR FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 314
SOFTWARE: PatentIn version 3.1
SEQ ID NO 48
LENGTH: 378
TYPE: PRT
ORGANISM: Homo sapiens
US-10-435-696-48

Query Match 99.2%; Score 1907; DB 15; Length 378;
Best Local Similarity 99.2%; Pred. No. 4,6e-157;
Matches 375; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDLGRPKMSVLLVALLVIFQVCLCODEVTDYIGNTTVDYTLFESLSCKDVRNFKAMF 60
DB 1 MDLGRPKMSVLLVALLVIFQVCLCODEVTDYIGNTTVDYTLFESLSCKDVRNFKAMF 60

QY 61 LPIWTSIIICFVGLGNGVLVLTYYIFKRLKMTDLYLNLAVADILFLTLTLPFMAYSAAK 120
DB 61 LPIWTSIIICFVGLGNGVLVLTYYIFKRLKMTDLYLNLAVADILFLTLTLPFMAYSAAK 120
QY 121 SWPFGVHFCKLIIFAIYKMSFSGMILLICISIDRYVAIVQAVSAHRHARVLLISKLSCV 180
DB 121 SWPFGVHFCKLIIFAIYKMSFSGMILLICISIDRYVAIVQAVSAHRHARVLLISKLSCV 180
QY 121 SWPFGVHFCKLIIFAIYKMSFSGMILLICISIDRYVAIVQAVSAHRHARVLLISKLSCV 180
DB 121 SWPFGVHFCKLIIFAIYKMSFSGMILLICISIDRYVAIVQAVSAHRHARVLLISKLSCV 180
QY 161 GSAILATVLSIPBELYSDLRSSSSQAMRCSLITEHVEAFITIOVAQWVIGFLVPLAMS 240
DB 161 GSAILATVLSIPBELYSDLRSSSSQAMRCSLITEHVEAFITIOVAQWVIGFLVPLAMS 240
QY 241 FCYLVIIITLLQARNFERKAKVILIAVVVFIYVQLPYNGVLAQTVANFNITSTCEL 300
DB 241 FCYLVIIITLLQARNFERKAKVILIAVVVFIYVQLPYNGVLAQTVANFNITSTCEL 300
QY 301 SKQNLIAVDVYSLACVRCNPFYAFIYKFRNDIFKLFQDLGCLSGEQLRQWSSCRH 360
DB 301 SKQNLIAVDVYSLACVRCNPFYAFIYKFRNDIFKLFQDLGCLSGEQLRQWSSCRH 360
QY 361 IRRSSMSVEAETTTTFSP 378
DB 361 IRRSSMSVEAETTTTFSP 378

RESULT 8

US-10-251-385-204
Sequence 204, Application US/10251385
Publication No. US20030105292A1
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. US20030105292A1-Endogenous, Constitutively Activated Human G
TITLE OF INVENTION: Protein-Coupled
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/10/251,385
CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: US/09/170,496
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: PatentIn version 3.1
SEQ ID NO 204
LENGTH: 378
TYPE: PRT
ORGANISM: Homo sapiens
US-10-251-385-204

Query Match 98.9%; Score 1900; DB 14; Length 378;
Best Local Similarity 98.9%; Pred. No. 1.9e-156;
Matches 374; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MDLGRPKMSVLLVALLVIFQVCLCODEVTDYIGNTTVDYTLFESLSCKDVRNFKAMF 60
DB 1 MDLGRPKMSVLLVALLVIFQVCLCODEVTDYIGNTTVDYTLFESLSCKDVRNFKAMF 60
QY 61 LPIWTSIIICFVGLGNGVLVLTYYIFKRLKMTDLYLNLAVADILFLTLTLPFMAYSAAK 120
DB 61 LPIWTSIIICFVGLGNGVLVLTYYIFKRLKMTDLYLNLAVADILFLTLTLPFMAYSAAK 120
QY 121 SWPFGVHFCKLIIFAIYKMSFSGMILLICISIDRYVAIVQAVSAHRHARVLLISKLSCV 180
DB 121 SWPFGVHFCKLIIFAIYKMSFSGMILLICISIDRYVAIVQAVSAHRHARVLLISKLSCV 180
QY 121 SWPFGVHFCKLIIFAIYKMSFSGMILLICISIDRYVAIVQAVSAHRHARVLLISKLSCV 180
DB 121 SWPFGVHFCKLIIFAIYKMSFSGMILLICISIDRYVAIVQAVSAHRHARVLLISKLSCV 180
QY 161 GSAILATVLSIPBELYSDLRSSSSQAMRCSLITEHVEAFITIOVAQWVIGFLVPLAMS 240
DB 161 GSAILATVLSIPBELYSDLRSSSSQAMRCSLITEHVEAFITIOVAQWVIGFLVPLAMS 240
QY 241 FCYLVIIITLLQARNFERKAKVILIAVVVFIYVQLPYNGVLAQTVANFNITSTCEL 300
DB 241 FCYLVIIITLLQARNFERKAKVILIAVVVFIYVQLPYNGVLAQTVANFNITSTCEL 300

QY 301 SKOLNIAVDYTTSLACVRCNPNPLVAFVGVKFRNDIFKLFKDLGCLISQOLRQWSSCRH 360
DB 301 SKOLNIAVDYTTSLACVRCNPNPLVAFVGVKFRNDIFKLFKDLGCLISQOLRQWSSCRH 360
QY 361 IRRSSMSVEAETTTTSP 378
DB 361 IRRSSMSVEAETTTTSP 378

RESULT 9

US-10-425-114-56811
Sequence 36811, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 56811
LENGTH: 475
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Clone ID: LIB4649-005-B4_Flt.pep
US-10-425-114-56811

Query Match 94.4%; Score 1814; DB 15; Length 475;
Best Local Similarity 98.9%; Pred. No. 6,9e-149;
Matches 355; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 20 QVCLCODEVTDDYIGNTTVDYTLFESLSKDVNRKAFPLPIMYSICFVGLNGLV 79
DB 117 KCLCODEVTDDYIGNTTVDYTLFESLSKDVNRKAFPLPIMYSICFVGLNGLV 176
QY 80 VLTYYFKLKTMTDYLNLAVADILFLTLFPMAYSAKSWFGVHFKLIPAIYKMS 139
DB 177 VLTYYFKLKTMTDYLNLAVADILFLTLFPMAYSAKSWFGVHFKLIPAIYKMS 236
QY 140 FRSGLMLLCISIDRYVAIVQAVSAHRHARVLLISLSCVSAIILATVLSPELLYSDL 199
DB 237 FRSGLMLLCISIDRYVAIVQAVSAHRHARVLLISLSCVSAIILATVLSPELLYSDL 296
QY 200 ORSSSSQARCSLITHEVEAFITIOVAQWVIGLVPLAMSFCYVITIRLLQARRPERN 259
DB 297 ORSSSSQARCSLITHEVEAFITIOVAQWVIGLVPLAMSFCYVITIRLLQARRPERN 356
QY 260 KAIKVIIVAVVVFIVFQLPYNGVLAQTVANFNITSTCELSKOLNIAVDYTTSLACVRC 319
DB 357 KAIKVIIVAVVVFIVFQLPYNGVLAQTVANFNITSTCELSKOLNIAVDYTTSLACVRC 416
QY 320 CNPPLVYAFVGVKFRNDIFKLFKDLGCLISQOLRQWSSCRHIRRSSMSVEAETTTTSP 378
DB 417 CNPPLVYAFVGVKFRNDIFKLFKDLGCLISQOLRQWSSCRHIRRSSMSVEAETTTTSP 475

RESULT 10

US-09-903-377-2
Sequence 2, Application US/09903377
Patent No. US20020116727A1
GENERAL INFORMATION:
APPLICANT: Allen, Keith D.
TITLE OF INVENTION: TRANSGENIC MICE CONTAINING CHEMOKINE
RECEPTOR 9A GENE DISRUPTIONS
FILE REFERENCE: R-365

QY 28 VDDYIGDMT-----VDYTLFESLSKDVNRKAFPLPIMYSICFVGLNGLV 82
DB 1 MADDYSESTSSMEDYVNFETDPCYCKNVHQPASHFLPPLVLFVIGALNSLVILV 60
QY 83 YIFKRLKTMTDYLNLAVADILFLTLFPMAYSAKSWFGVHFKLIPAIYKMSFES 142
DB 61 YKCTRVKTMDFLNLAIADILFLTLFPMAYSAKSWFGVHFKLIPAIYKMSFES 120
QY 143 GMLLCISIDRYVAIVQAVSAHRHARVLLISLSCVSAIILATVLSPELLYSDLORS 202
DB 121 CVLLIMCISVDRYVAIVQAVSAHRHARVLLISLSCVSAIILATVLSPELLYSDLORS 180
QY 203 SSEQARCSLI-----THEVEAFITIOVAQWVIGLVPLAMSFCYVITIRLLQARR 256
DB 181 SG--IAICTWVPSPDESTKLSAVLTKV--ILGFLPVAWVACCTYIIHTLIQAKS 235
QY 257 ERKAIKVIIVAVVVFIVFQLPYNGVLAQTVANFNITSTCELSKOLNIAVDYTTSLAC 316
DB 236 SKKAIKVIIVAVVVFIVFQLPYNGVLAQTVANFNITSTCELSKOLNIAVDYTTSLAC 295
QY 317 VRCVNPPLVYAFVGVKFRNDIFKLFKDLGCLISQOLRQWSSCRH---IRRSSMSVE 369
DB 296 FRSCLNPVLYVFGVFRNDIFKLFKDLGCLISQOLRQWSSCRH---IRRSSMSVE 349

RESULT 11

US-09-952-385-2
Sequence 2, Application US/09952385
Patent No. US20020119504A1
GENERAL INFORMATION:
APPLICANT: Andrew, David P.
APPLICANT: Zabel, Brian A.
APPLICANT: Ponath, Paul D.
TITLE OF INVENTION: ANTI-GRP-9-6 ANTIBODIES AND METHODS OF
FILE REFERENCE: IKS98-16
CURRENT APPLICATION NUMBER: US/09/952,385
CURRENT FILING DATE: 2001-09-13
PRIOR APPLICATION NUMBER: 09/266,464
PRIOR FILING DATE: 1999-03-11
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 357
TYPE: PRT
ORGANISM: Homo sapiens
US-09-952-385-2

Query Match 39.5%; Score 758.5; DB 9; Length 357;
Best Local Similarity 42.0%; Pred. No. 1.7e-57;
Matches 150; Conservative 78; Mismatches 106; Indels 23; Gaps 6;

Qy	28	VTQDYEJGNT-----VDYTLFESLCSKQDVRFKMFPIIMISICFPGLLGNGVLT	82
Db	1	MADDYGESESSMEDYVNFNFPTDPCYKKNVQFASHFLPELTYWLVFYGALGNSLVLY	60
Qy	83	YIYFKRLKMTDITLYLNLAVADILPLTLPEFMAYSAAKSMWGVHCECKLIFAYIKMSPS	14
Db	61	YWCCTRVKMTDMFNLMLAIADLFLVTLPEFMAIADQMKFQTFCKYVNSWYKKNFYS	12
Qy	143	GMLLLCTSIDRVAIVQAVSARHHRVLLISKLSCVGSAILATYLSIPELLYDLQBS	20
Db	121	CYLLIMCISVDRYAIALQAMRAHTWREKRLYLSKWCFTIWTYLAALCIPELIYSQIKE	18
Qy	203	SSEQARMCSLI-----TEHVEAFITTYQAQWYIGTVLPLMSFCYLYITRTLOARNF	25
Db	181	SG--IALCTWYPSDESTYKLSKASVLTUK---ILGFPLFPYVWACCYTTIIHITLQAKKS	23
Qy	257	ERKKAIIVIIIAVVVVFVLPQLPNGVVLQGVANENITSTOEKQLMIADVYSLAC	31
Db	236	SKHQLKVTITVIVLFPALSQFPNLCILVTTIDVAVMPTISNCVSTINDICQVQYTLAF	29
Qy	317	VRCCVNFELFAYIGVKFRNDIFXLFKDLGCLSQEQRLQMSCRH-----IRRSMSVE	369
Db	296	FHGLTNFVLVYFGERFRRLVYTKLNGCISQ---AQWVSFRRREGSLKLSMILE	349

```

RESULT 12
US-09-966-755-2
; Sequence 2, Application US/09966755
; Publication No. US20030022238A1
; GENERAL INFORMATION:
; APPLICANT: Andrew, David P.
; APPLICANT: Zabel, Brian A.
; APPLICANT: Pomath, Paul D.
; TITLE OF INVENTION: ANTI-GPR-9-6 ANTIBODIES AND METHODS OF
; TITLE OF INVENTION: IDENTIFYING AGENTS WHICH MODULATE GPR-9-6 FUNCTION
; FILE REFERENCE: LKS98-16
; CURRENT APPLICATION NUMBER: US/09/966,755
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/266,464
; PRIOR FILING DATE: 1999-03-11
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-966-755-2

```

[illegible]

Qy 317 VRCVNPFLYAFIGVKFRNDIFKLFRODGLCSOEQLRWSSCH---IRRSSSVE 369
 :|||:::||:|||||: |||:
 Db 296 FHSCINPVLYFVGERRRDLVTKLNLGCSIQ--AQWVSPTRRREGSLKLSSMLE 349

```

RESULT 13
US-10-000-759A-2
: Sequence 2, Application US/10000759A
: Publication No. US20020141991A1
: GENERAL INFORMATION:
: APPLICANT: Andrew, David P.
: APPLICANT: Zabel, Brian A.
: APPLICANT: Ponath, Paul D.
: TITLE OF INVENTION: ANTI-GPR-9-6 ANTIBODIES AND METHODS OF
: TITLE OF INVENTION: IDENTIFYING MODULATORS OF GPR-9-6 FUNCTION
: FILE REFERENCE: 185.1064-003
: CURRENT APPLICATION NUMBER: US/10/000.759A
: CURRENT FILING DATE: 2001-10-23
: PRIOR APPLICATION NUMBER: US/09/522,752
: PRIOR FILING DATE: 2000-05-10
: PRIOR APPLICATION NUMBER: US 09/266,464
: PRIOR FILING DATE: 1999-03-11
: NUMBER OF SEQ ID NOS: 15
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 2
: LENGTH: 357
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-10-000-759A-2

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	Query Match	39.5%	Score 758.5; DB 13;	Length 357;
	Best Local Similarity	42.0%;	Pred. No. 1.7e-57;	
	Matches 150;	Conservative	78; Mismatches 166;	Indels 23; Gaps 6;
Qy	28 VTDDYIGDNTT-----VDYTLFESLCSKDKVRNFKAMFLPIMYSIICFVGLNGELVLVT	82		
Db	1 MADDYGESSTSMEDYNFNFTDFCEKNRVGASHFLPELTWLTVFVGALGNSLVITLV	60		
Qy	83 YIYRKLTMTDTYTLMLAVADILFLTLPPWASAKSWFGHCFCLTAITYKMSPFS	142		
Db	61 YMCTRYKXTMDMFLMLAIADLLFLTLPFWAIIAADQMKEQFMCCVNWSMYKKMYS	120		
Qy	143 GMILLTCISIDRYYAIVQAVSAHHRRARVLLISTLCSGAIIATVLSIPELTSIDLORS	202		
Db	121 CVALIMCISVDRIYAIAOMAPAHARWRERKLYSKVCETTVLAALCIPELTSIQIEE	180		
Qy	203 SSEOAMECSLI-----TEHEAEITIOVAMVIGFLVPFLMASFCYLVIIRTLLOARNF	256		
Db	181 SG--IALCTMWYPDESKLKSAVLTLYK---ILGFLEPVVMACCVYIIHTLLIQAKKS	235		
Qy	257 ERNKAIKYIIAAVVVFVIFQLPNGVAVLAQTVANFNITSSTCELASKOLNIAYDTYSLAC	316		
Db	236 SKHKALKVTITVLTVFPLSOPPCYNCILVOTIIDYAFMEISCAVSTINDICEFOYTOTIAF	295		
Qy	317 VRCVNFELFAIGVKFRNDIFKLFXDLGCSQSOLRWSSCRH----IRRSSSVE	369		
Db	296 FHSCLNPFLVYVERFRRLVKTLKDLGCISQ---ADMVSPTTRBSGLKASSMLLE	349		

```

RESULT 14
US-10-251-385-24
; Sequence 24, Application US/10251385
; Publication No. US20030105292A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. US20030105292A1-Endogenous, Constitutively Activated Human G
; TITLE OF INVENTION: Protein-Coupled
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/10/251,385
; CURRENT FILING DATE: 2002-09-20

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PRIOR APPLICATION NUMBER: US/09/170,496
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: PatentIn version 3.1
SEQ ID NO 24
LENGTH: 357
TYPE: PRT
ORGANISM: Homo sapiens
US-10-251-385-24

Query Match 39.5%; Score 758.5; DB 14; Length 357;
Best Local Similarity 42.0%; Pred. No. 1.7e-57;
Matches 150; Conservative 78; Mismatches 106; Indels 23; Gaps 6;

QY 28 VTDDYIGDNTT-----VDYTLFESLCSKDVNRPKAFPLPIMYSIICFVGLGSLVLT 82
DB 1 MADDYGESTSSMEDYVNFPTDPCKNVRQPSHFPLPYLVIVIGALGSLVIV 60
QY 83 YIYFKRLKMTDTYLLNLAVADILFLLTLPFMVSAKSVFVGFCKLIIPAIYKMSFFS 142
DB 61 YWYCTRVKMTDMFLNLAIADLLFLVTLFPMVIAADQWKQFTFMCKVNSMYKMFYS 120
QY 143 GMLLLCISIDRYVAIVQAVSAHRHRARVLLISLSCVGSAILATVSIPELVSDDLQRS 202
DB 121 CVLLIMCISVDRYIALAQAMRAHTWRKRLYSKMCFTIWLVAALCIPBILYSQIKER 180
QY 203 SSEQARCSLI-----TEHVEAFITQVAMVIGFLVPLPMSFCYLVIRTLQARNF 256
DB 181 SG--IAICTMNVPSDESTYKLSAVLTIKV---ILGFPLPVVMACTYIIITLQAKS 235
QY 257 ERNKAIKVIAVAVVFLVFLQVPGVLAQTVANFNITSSTCELSKQNLAYDVTSYLAC 316
DB 236 SKKALKVITVTLVFLVLSQFPYNCILVQTDAYAMFISNCAVSTNIDICFOVTQTIAR 295
QY 317 VRCCVNPFLYAFIGVKFRNDIFKLFRDLGCLSQEQLRQWSSCRH---IRSSMSVE 369
DB 296 FHSCLNPVLVYFVGERFRRLDVTKLNIGCISQ---AQWVSFTRRBSLKLSSMLE 349

RESULT 15

US-10-225-567A-241
Sequence 241, Application US/10225567A
Publication No. US2003013798A1
GENERAL INFORMATION:
APPLICANT: Lifespan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Burnet, Glenn C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 292
SOFTWARE: PatentIn version 3.1
SEQ ID NO 241
LENGTH: 357
TYPE: PRT
ORGANISM: Homo sapiens
US-10-225-567A-241

Query Match 39.5%; Score 758.5; DB 14; Length 357;
Best Local Similarity 42.0%; Pred. No. 1.7e-57;
Matches 150; Conservative 78; Mismatches 106; Indels 23; Gaps 6;

QY 28 VTDDYIGDNTT-----VDYTLFESLCSKDVNRPKAFPLPIMYSIICFVGLGSLVLT 82
DB 1 MADDYGESTSSMEDYVNFPTDPCKNVRQPSHFPLPYLVIVIGALGSLVIV 60
QY 83 YIYFKRLKMTDTYLLNLAVADILFLLTLPFMVSAKSVFVGFCKLIIPAIYKMSFFS 142
DB 61 YWYCTRVKMTDMFLNLAIADLLFLVTLFPMVIAADQWKQFTFMCKVNSMYKMFYS 120

QY 143 GMLLLCISIDRYVAIVQAVSAHRHRARVLLISLSCVGSAILATVSIPELVSDDLQRS 202
DB 121 CVLLIMCISVDRYIALAQAMRAHTWRKRLYSKMCFTIWLVAALCIPBILYSQIKER 180
QY 203 SSEQARCSLI-----TEHVEAFITQVAMVIGFLVPLPMSFCYLVIRTLQARNF 256
DB 181 SG--IAICTMNVPSDESTYKLSAVLTIKV---ILGFPLPVVMACTYIIITLQAKS 235
QY 257 ERNKAIKVIAVAVVFLVFLQVPGVLAQTVANFNITSSTCELSKQNLAYDVTSYLAC 316
DB 236 SKKALKVITVTLVFLVLSQFPYNCILVQTDAYAMFISNCAVSTNIDICFOVTQTIAR 295
QY 317 VRCCVNPFLYAFIGVKFRNDIFKLFRDLGCLSQEQLRQWSSCRH---IRSSMSVE 369
DB 296 FHSCLNPVLVYFVGERFRRLDVTKLNIGCISQ---AQWVSFTRRBSLKLSSMLE 349

Search completed: February 25, 2005, 02:35:30
Job time: 136 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 25, 2005, 02:14:37 ; Search time 40 Seconds
(without alignments)
909,248 Million cell updates/sec

Title: US-10-749-990-2

Sequence: 1 MDLGRKMSVLLVALLVIFQ.....RHRRSSMSVEAEITTTTSP 378

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1922	100.0	378	2	A45680 G protein-coupled
2	1907	99.2	378	2	B55735 lymphocyte-specific
3	1696	88.2	378	2	A55735 G protein-coupled
4	707.5	36.8	369	2	UC5068 G protein-coupled
5	618	32.2	350	2	JN0621 G protein-coupled
6	614	31.9	360	2	A57160 chemokine (C-C) re
7	595	31.0	360	2	UC4587 chemokine (C-C) re
8	574	29.9	327	2	SS6162 MDCR15 protein - h
9	574	29.9	358	2	A53752 interleukin-8 rece
10	574	29.9	372	2	S26667 G protein-coupled
11	570.5	29.7	367	2	JB0349 interferon-gamma
12	570	29.7	374	2	J18450 chemokine (C-C) re
13	567.5	29.5	360	2	JC2443 chemokine (C-C) re
14	565	29.4	355	2	JQ1231 interleukin-8 rece
15	562.5	29.3	374	2	S42628 G protein-coupled
16	561.5	29.2	360	2	A53611 interleukin-8 rece
17	556.5	29.0	374	2	S32785 G protein-coupled
18	553.5	28.8	355	2	A45177 chemokine (C-C) re
19	553	28.8	352	2	A43113 chemokine (C-C) re
20	549.5	28.6	353	2	S28787 neuropeptide Y/pep
21	539	28.0	359	2	A48921 interleukin-8 rece
22	538	28.0	352	2	A45747 neuropeptide Y/pep
23	533	27.7	350	2	A39445 interleukin-8 rece
24	530.5	27.6	356	2	S42096 interleukin-8 rece
25	529	27.5	359	2	A49341 MIP-1 alpha recept
26	525	27.3	352	2	G00048 fusin (FUSIN) - C
27	524.5	27.3	355	2	G02436 chemokine (C-C) re
28	524.5	27.3	383	2	SS5594 G protein-coupled
29	522	27.2	354	2	B55733 G protein-coupled

30	509.5	26.5	355	2	I49339 macrophage inflam
31	500	26.0	355	2	JC5067 G protein-coupled
32	482.5	25.1	355	2	UC4304 orphan G protein-c
33	478.5	24.9	356	2	I49340 MIP-1 alpha recept
34	477.5	24.8	354	2	A23669 interleukin-8 rece
35	477	24.8	354	2	I58186 probable G protein
36	441.5	23.0	362	2	UN0694 angiotensin II rec
37	434	22.6	359	2	S15403 angiotensin II rec
38	433.5	22.6	359	2	A42656 angiotensin II rec
39	433	22.5	359	2	S44425 angiotensin II rec
40	430	22.4	359	2	JC1104 angiotensin II rec
41	429	22.3	359	2	JC2134 angiotensin II rec
42	428	22.3	359	2	JC1194 angiotensin II rec
43	426.5	22.1	359	2	J01516 angiotensin II rec
44	424	22.1	359	2	A48857 angiotensin II rec
45	423	22.0	359	2	JH0621 angiotensin II rec

ALIGNMENTS

RESULT 1

A45680 G protein-coupled peptide receptor BBI 1 - human

C/Species: Homo sapiens (man)

C/Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C/Accession: A45680

R/Birkenbach, M.; Josefsen, K.; Yalamanchili, R.; Lenoir, G.; Kieff, E.

U. Virol. 67, 2209-2220, 1993

A/Title: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-coupled p

A/Reference number: A45680; PMID:93188173; PMID:8383238

A/Accession: A45680

A/Status: preliminary

A/Molecule type: nucleic acid

A/Residues: 1-378 <IR>

A/Cross-references: UNIPROT: P32248; GB: I08176; NID: G183484; PID: G183485

A/Experimental source: B-lymphocytes

A/Note: sequence extracted from NCBI backbone (NCBIN:127094, NCBI:P.127095)

C/Superfamily: vertebrate rhodopsin

C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match 100.0%; Score 1922; DB 2; Length 378;
Best Local Similarity 100.0%; Pred. No. 8e-153;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MDLGRKMSVLLVALLVIFQVCLQDBVTDDYIGDNTVDYTLFESLCSKQDVRNFRAMP	60
DB	1	MDLGRKMSVLLVALLVIFQVCLQDBVTDDYIGDNTVDYTLFESLCSKQDVRNFRAMP	60
QY	61	LPIMYSIIICFVGLGNGLVLTIVYFKRLKTMVDTYLLMLAVADILFLTLPPMAYSAK	120
DB	61	LPIMYSIIICFVGLGNGLVLTIVYFKRLKTMVDTYLLMLAVADILFLTLPPMAYSAK	120
QY	121	SWFVGVPCKLIPAIYKMSFPGMLLLCISIDRYVAIVQASARHRRARVLLISKLSV	180
DB	121	SWFVGVPCKLIPAIYKMSFPGMLLLCISIDRYVAIVQASARHRRARVLLISKLSV	180
QY	181	GSAILTAVLSIPBLVSDIQRSSSEQAMRCSLTTEVEAFITTVQVQWYIGFVPLLAWS	240
DB	181	GSAILTAVLSIPBLVSDIQRSSSEQAMRCSLTTEVEAFITTVQVQWYIGFVPLLAWS	240
QY	241	FCVLVIRTLQARFERNKAIKVIIVAVVFIPOLPNGVLLAQTVAINFITSSSTCEL	300
DB	241	FCVLVIRTLQARFERNKAIKVIIVAVVFIPOLPNGVLLAQTVAINFITSSSTCEL	300
QY	301	SKQNLAVDVYTSIACVRCVNPFLVAFGVKFRNDIFKLFDLGLSGLQSDQLRQMSCRH	360
DB	301	SKQNLAVDVYTSIACVRCVNPFLVAFGVKFRNDIFKLFDLGLSGLQSDQLRQMSCRH	360
QY	361	IRRSSMSVEAEITTTTSP 378	
DB	361	IRRSSMSVEAEITTTTSP 378	

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RESULT 2
B55735
Lymphocyte-specific G protein-coupled receptor EB1 - human
N:Alternate names: Burkitt's lymphoma receptor 2; Epstein-Barr virus induced protein 1
C:Species: Homo sapiens (man)
C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C:Accession: B55735; S52443
R:Schweickart, V.L.; Raport, C.U.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.
Genomics 23, 643-650, 1994
A:Title: Cloning of human and mouse EB1, a lymphoid-specific G-protein-coupled receptor
A:Reference number: A55735; MUID:95154835; PMID:7851893
A:Accession: B55735
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-378 <SCH>
A:Cross-references: UNIPROT:P32248; GB:L31581; NID:9468319; PIDN:AAA7423.1; PID:9468320
R:Burstchler, R.; Kempkes, B.; Staube, K.; Lipp, M.
submitted to the EMBL Data Library, February 1995
A:Description: The expression of the chemokine receptor BLR2/EB1 is specifically trans
A:Reference number: S52443
A:Accession: S52443
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 21-378 <BUR>
A:Cross-references: EMBL:X84702
C:Genetics:
A:Gene: GDB:CMKBR7; EB11; BLR2; CCR7
A:Cross-references: GDB:342065; OMIM:600242
A:Map position: 17q12-17q21.2
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor

Query Match      99.2%; Score 1907; DB 2; Length 378;
Best Local Similarity 99.2%; Pred. No. 1.4e-151;
Matches 375; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDLGRPKMSVLLVALLVIFQVCLCODEVTDDYIGDNTTYDYLTFESLCSKQVRNFKAMF 60
DB 1 MDLGRPKMSVLLVALLVIFQVCLCODEVTDDYIGDNTTYDYLTFESLCSKQVRNFKAMF 60
QY 61 LPIWYSIICFVGLGNGVLVLTYYIFPKRLKMTDPTLLNLAAVDILFLITLPPMAVSAK 120
DB 61 LPIWYSIICFVGLGNGVLVLTYYIFPKRLKMTDPTLLNLAAVDILFLITLPPMAVSAK 120
QY 121 SWPFGVHCKLIIFALYKMSFSGMILLICISIDRYVAIVQAVSAHRHARVLLISLSCV 180
DB 121 SWPFGVHCKLIIFALYKMSFSGMILLICISIDRYVAIVQAVSAHRHARVLLISLSCV 180
QY 181 GSAILATVLSIPELLVSDLQSSSSSEQAMRCSLITEHVEAFITIQVAQWVIGFLVPLAMS 240
DB 181 GSAILATVLSIPELLVSDLQSSSSSEQAMRCSLITEHVEAFITIQVAQWVIGFLVPLAMS 240
QY 241 FCYLVITRTLLQARNPERNKAIKVIIVAVVVFIPQLPNGVLAQTVAENFNTSSGTEL 300
DB 241 FCYLVITRTLLQARNPERNKAIKVIIVAVVVFIPQLPNGVLAQTVAENFNTSSGTEL 300
QY 301 SKQLNIADVYTSLSACVCCVNPFLYAFIGVFRNDIFKLPDGLCSOELROMSSCRH 360
DB 301 SKQLNIADVYTSLSACVCCVNPFLYAFIGVFRNDIFKLPDGLCSOELROMSSCRH 360
QY 361 IRRSSMSVEAETTTTFFSP 378
DB 361 IRRSSMSVEAETTTTFFSP 378

RESULT 3
A55735
G protein-coupled receptor EB11 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C:Accession: A55735
R:Schweickart, V.L.; Raport, C.U.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.
```

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Genomics 23, 643-650, 1994
A:Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor
A:Reference number: A55735; MUID:95154835; PMID:7851893
A:Accession: A55735
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-378 <SCH>
A:Cross-references: UNIPROT:P47774; GB:L31580; NID:9468340; PIDN:AAA7423.1; PID:9468341
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor

Query Match      88.2%; Score 1696; DB 2; Length 378;
Best Local Similarity 86.0%; Pred. No. 5.7e-134;
Matches 325; Conservative 27; Mismatches 26; Indels 0; Gaps 0;

QY 1 MDLGRPKMSVLLVALLVIFQVCLCODEVTDDYIGDNTTYDYLTFESLCSKQVRNFKAMF 60
DB 1 MDLGRPKMSVLLVALLVIFQVCLCODEVTDDYIGDNTTYDYLTFESLCSKQVRNFKAMF 60
QY 61 LPIWYSIICFVGLGNGVLVLTYYIFPKRLKMTDPTLLNLAAVDILFLITLPPMAVSAK 120
DB 61 LPIWYSIICFVGLGNGVLVLTYYIFPKRLKMTDPTLLNLAAVDILFLITLPPMAVSAK 120
QY 121 SWPFGVHCKLIIFALYKMSFSGMILLICISIDRYVAIVQAVSAHRHARVLLISLSCV 180
DB 121 SWPFGVHCKLIIFALYKMSFSGMILLICISIDRYVAIVQAVSAHRHARVLLISLSCV 180
QY 181 GSAILATVLSIPELLVSDLQSSSSSEQAMRCSLITEHVEAFITIQVAQWVIGFLVPLAMS 240
DB 181 GSAILATVLSIPELLVSDLQSSSSSEQAMRCSLITEHVEAFITIQVAQWVIGFLVPLAMS 240
QY 241 FCYLVITRTLLQARNPERNKAIKVIIVAVVVFIPQLPNGVLAQTVAENFNTSSGTEL 300
DB 241 FCYLVITRTLLQARNPERNKAIKVIIVAVVVFIPQLPNGVLAQTVAENFNTSSGTEL 300
QY 301 SKQLNIADVYTSLSACVCCVNPFLYAFIGVFRNDIFKLPDGLCSOELROMSSCRH 360
DB 301 SKQLNIADVYTSLSACVCCVNPFLYAFIGVFRNDIFKLPDGLCSOELROMSSCRH 360
QY 361 IRRSSMSVEAETTTTFFSP 378
DB 361 IRRSSMSVEAETTTTFFSP 378

RESULT 4
JCS068
G protein-coupled receptor CKR-L3 - human
C:Species: Homo sapiens (man)
C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000
C:Accession: JCS068
R:Zabablos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.
Biochem. Biophys. Res. Commun. 227, 846-853, 1996
A:Title: Molecular cloning and RNA expression of two new human chemokine receptor-like ge
A:Reference number: JCS067; MUID:97040707; PMID:8886020
A:Accession: JCS068
A:Molecule type: DNA
A:Residues: 1-369 <ZAB>
A:Cross-references: EMBL:Z79784; NID:91668737; PIDN:CA802144.1; PID:91668738
C:Comment: This protein belongs to the family of alpha chemokine receptors.
C:Genetics:
A:Gene: GDB:CMKBR6; STRL22; GPR29; CCR6; CKR-L3; GPR-CY4
A:Cross-references: GDB:5370639; OMIM:601835
A:Map position: 6q27-q27
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein
F:42-68/Domain: transmembrane #status predicted <TM1>
F:79-99/Domain: transmembrane #status predicted <TM2>
F:115-136/Domain: transmembrane #status predicted <TM3>
F:160-180/Domain: transmembrane #status predicted <TM4>
F:212-233/Domain: transmembrane #status predicted <TM5>
F:250-271/Domain: transmembrane #status predicted <TM6>
F:292-315/Domain: transmembrane #status predicted <TM7>
```


Query Match 36.8%; Score 707.5; DB 2; Length 369;
Best Local Similarity 42.7%; Pred. No. 1.6e-51;
Matches 153; Conservative 75; Mismatches 115; Indels 15; Gaps 7;

QY 26 DEVTDDYIGDNT---TVDYTLFESLCSKQDVNRKFMFLPIMYSIICFVGLNGVLVLT 82
DB 8 DSEEDFVSVNYSYVSDSEML--LCSLQEQFQSRFLFPIAIVSLICVFLNINILVIT 65
QY 83 YIFKRLKMTDTYLLNLAVADILFLTLFPMAVS--AAKSWFGVHFCKLIPAIYKMSFF 141
DB 66 FAFYKARSMTDVYLLNMAADILFLTLFPMAVSHATGMVNSMACKLIGIYAINFN 125
QY 142 SGMILLICISIDRYVAIVQAVSAHRHARVLLISKLSVGSAILATVLSIPELYSDLQR 201
DB 126 CGMLLTCTISMDRYIAIVQATKSPRLSRITLPSRKIIICLVWGLSVLISSSTFVFN--QK 183
QY 202 SSSQAMRC---SLTTEHBAFTTVOAGVIGFLVPLAMSPCYIITRTLLQARNE 257
DB 184 YNTQSDVCEPKYQTVSEPIRMKLMGLLELFGFPIPLMFMFICYPIYKTIWQAMNSK 243
QY 258 RNKAIKIIIVAVVFIYFQLPYNGVLAQTVAANFNITSSTCELSKOLINAVDYSLACV 317
DB 244 RHRKAIIVIAVAVFLACQIPHN--MULLVTANLIGKMRSCQSBKLIIGTKYITVLAFL 302
QY 318 RCCVNPFLYAVIGVFRNDIFKLPKQGLCSQEQRLQWSSCRHIRSSMSVBAETTTT 375
DB 303 HCLINPVLVAFIQGRFRNYPFLKILKQDMCVRRYKSGGFC--AGRYSENISSOTSRT 358

RESULT 5

JN0621
G protein-coupled receptor type B - bovine
C/Species: Bos primigenius taurus (cattle)
C/Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C/Accession: JN0621
R/Matsuoka, I.; Mori, T.; Aoki, J.; Sato, T.; Kurihara, K.
Biochem. Biophys. Res. Commun. 194, 504-511, 1993
A/Title: Identification of novel members of G-protein coupled receptor superfamily
A/Reference number: JN0621, PMID:93326166; PMID:8392843
A/Accession: JN0621
A/Molecule type: mRNA
A/Residues: 1-350 <TM>
A/Cross-references: UNIPROT:P35350; GB:563848; NID:g939710; PIDN:AAAB2547.1; PID:g939711
A/Experimental source: tongue taste papillae
C/Comment: This protein is involved in modulating taste sensitivity or regeneration of
C/Superfamily: vertebrate rhodopsin
C/Keywords: G protein-coupled receptor; glycoprotein; receptor; transmembrane protein
F/42-66/Domain: transmembrane #status predicted <TM2>
F/80-99/Domain: transmembrane #status predicted <TM2>
F/114-135/Domain: transmembrane #status predicted <TM3>
F/154-175/Domain: transmembrane #status predicted <TM4>
F/200-222/Domain: transmembrane #status predicted <TM5>
F/242-265/Domain: transmembrane #status predicted <TM6>
F/284-306/Domain: transmembrane #status predicted <TM7>
F/6,19/Binding site: carbohydrate (Aan) (covalent) #status predicted

Query Match 32.2%; Score 618; DB 2; Length 350;

Best Local Similarity 36.8%; Pred. No. 4.5e-44;
Matches 135; Conservative 70; Mismatches 124; Indels 38; Gaps 8;

QY 26 DEVTDDYIGD---NTVDYTLFESLCSKQDVNRKFMFLPIMYSIICFVGLNGVLVLT 82
DB 6 NGSTDYVYENENNDTHDSQYEVICKEBVRKPAKFLPAPPTIAFIIDLAGNSTVVAI 65
QY 83 YIFKRLKMTDTYLLNLAVADILFLTLFPMAVSAAKSWFGVHFCKLIPAIYKMSFFS 142
DB 66 YAYYKRRRTDYYIINLAADLFLTLFPMAVNAHGVNLGIMCKVTSALYTNFVS 125
QY 143 GMLLICISIDRYVAIVQAVSAHRHARVLLISKLSVGSAILATVLSIPELYSDLQRS 202
DB 126 GMPFLACISIDRYVAIVQAVSAHRHARVLLISKLSVGSAILATVLSIPELYSDLQRS 202
QY 203 SSSQAMRC-SLTTEHBAFTTVOAGVIGFLVPLAMSPCYIITRTLLQARNE 259

DB 182 A-----RCVPDFPHYHGTSMKASIQILEICIGIIFPLMAVCFYITAKTLIKMPNKK 236
QY 260 KAIKIIIVAVVFIYFQLPYNGVLAQTVAANFNITSSTCELSKOLINAVDYSLACVRC 319
DB 237 QPLKVLFTVYIVIVQLPYNIVKFCOADIYISLTDCMSKMDVAITITESIALFHS 236
QY 320 CVNPFLYAVIGVFRNDIFKLPKQGLCSQEQRLQWSSCRHIRSSMSVBAETTTT 370
DB 297 CLNPFLYVFMGTSFKNYIMKVAKKYG-----SW-----RRQGNVBEIPESEDA 342
QY 371 ETTTTPS 377
DB 343 EPTSTPS 349

RESULT 6

A57160
Chemokine (C-C) receptor 4 - human
N/Alternate names: C-C CKR-4
C/Species: Homo sapiens (man)
C/Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C/Accession: A57160
R/Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogwerf, A.J.; Proudfoot, A.E.I.; We
J. Biol. Chem. 270, 19495-19500, 1995
A/Title: Molecular cloning and functional expression of a novel CC chemokine receptor cdt
A/Reference number: A57160, PMID:95370289; PMID:7642634
A/Accession: A57160
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-360 <POW>
A/Cross-references: UNIPROT:P51679; GB:X85740; NID:g1370103; PIDN:CAAS9743.1; PID:g97145;
A/Note: source clone KS-5
C/Genetics:
A/Gene: GDB:CMKBR4
A/Cross-references: GDB:677463
A/Map position: 3p21-3p21
C/Superfamily: vertebrate rhodopsin
C/Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prote
F/40-65/Domain: transmembrane #status predicted <TM1>
F/76-97/Domain: transmembrane #status predicted <TM2>
F/112-133/Domain: transmembrane #status predicted <TM3>
F/151-175/Domain: transmembrane #status predicted <TM4>
F/208-226/Domain: transmembrane #status predicted <TM5>
F/243-264/Domain: transmembrane #status predicted <TM6>
F/291-308/Domain: transmembrane #status predicted <TM7>
F/29-276,110-187/Disulfide bonds: #status predicted
F/72,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
F/145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F/183,194/Binding site: carbohydrate (Aan) (covalent) #status predicted
F/321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 31.9%; Score 614; DB 2; Length 360;

Best Local Similarity 39.3%; Pred. No. 1e-43;
Matches 126; Conservative 75; Mismatches 110; Indels 10; Gaps 5;

QY 27 EYTDYVIGNTYDYLTFESL---CSKQDVNRKFMFLPIMYSIICFVGLNGVLVLT 83
DB 5 DINDTLLDSIYSNLYVESIPKCTKRGKAGELFPLPLSLVTVFVGLSGSVVVLV 64
QY 84 IYFKRLKMTDTYLLNLAVADILFLTLFPMAVSAAKSWFGVHFCKLIPAIYKMSFFSG 143
DB 65 FKXKRLRSMTDYLLNLAVADILFLTLFPMAVNAHGVNLGIMCKVTSALYTNFVS 124
QY 144 MLLLICISIDRYVAIVQAVSAHRHARVLLISKLSVGSAILATVLSIPELYSDDLQR 201
DB 125 IFFVWMLMSIDRYVAIVQAVSAHRHARVLLISKLSVGSAILATVLSIPELYSDDLQR 201
QY 202 SSSQAMRC-SLTTEHBAFTTVOAGVIGFLVPLAMSPCYIITRTLLQARNE 261
DB 183 NHTYCTKSLNSTTWKVLSSLEI--NITGLVPLDILMFCYSWITRTLLQARNE 240
QY 262 IKVIAVAVVFIYFQLPYNGVLAQTVAANFNITSSTCELSKOLINAVDYSLACVRCV 321

Db 21 VAMTAAVAVVLEGFMTPTNIVFLFETLVELEVLQD-CFPERLYDAIQETTLAFVHCL 299
Qy 322 NPFLYAFGVKFRNDIFKLFK 342
Db 300 NPILYFPLGEKFRKYLQLFK 320

RESULT 7
JC4587
chemokine (C-C) receptor 4 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C:Accession: J04587
R:Hoogewerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.
Biochem. Biophys. Res. Commun. 218, 337-343, 1996
A:Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to
A:Reference number: J04587; MUID:96136324; PMID:8573157
A:Accession: J04587
A:Molecule type: mRNA
A:Residues: 1-360 <HOO>
A:Cross-references: UNIPROT:P51680; EMBL:X90862; NID:g1167851; PIDN:CAA62372.1; PID:g116
A:Experimental source: thymus
C:Genetics:
A:Gene: CC CKR-4
C:Superfamily: vertebrate rhodopsin
C:Keywords: glycoprotein; phosphoprotein; receptor; thymus
F:2,183,194/Binding site: carboxydrate (Asn) (covalent) #status predicted
F:72,202,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status pred
F:145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 31.0%; Score 595; DB 2; Length 360;
Best Local Similarity 35.9%; Pred. No. 3.9e-42;
Matches 133; Conservative 72; Mismatches 121; Indels 44; Gaps 8;

Qy 27 EYTDYIGNTVDYTLFESL---CSKQDVRFKAMPFIPMYSIICFVGLNGLVLT 83
Db 5 EYTDYTDQETVNSYFYSMMPCKTKEGKAFGEVFLPPLSLVFLGLFGNSVVVL 64

Qy 84 IYFKRLKMTDTYLLNLAVADILFLTPFMAYSAKSWFVHFCXLIFAIYKMSFSG 143
Db 65 FYKRLKMTDTYLLNLASDLFLTPFMSYADQVDFGLCKIYSMTLVGFYSG 124

Qy 144 MLLLCISIDRYVAIVQAVSAHRHARVLLISLSCVGSAILATVLSIPELLSDQRSS 203
Db 125 IFPIMMSIDRYLAIVHAVFS--LKARLTLYGVITSLITMSVAVFASLPGLFS----- 176

Qy 204 SQQMRCSLITHEVAFTIQAQ-----WYIGFLVPLAMSFCYLVIRTL 250
Db 177 -----TCYTEHNTYCKTQYSVNSTWKLSSLEINVLGLIPGLMFWYSMTIRTL 229

Qy 251 IQARPERKAIKVIIVAVVPIVFPOLPYNGVLAQTVANFITSCTELSKOLNAYDV 310
Db 230 QICKKEKRRARVRLFGVVFLFGFTPTYNVFLFETLVELEVLQD-CLLEKLYDAIQA 288

Qy 311 TYSLACVRCVNPFLYAFIVGVKFRNDIFLKFQDGLSGOGLROWSSCRH-----IRRS 365
Db 289 TETLGFHCCINPVIYFPLGEKFRKYLQLFK--CRGPLV-----CGHCPLOYASAD 341

Qy 366 MSVEAETTT 375
Db 342 MSSSYTOST 351

RESULT 8
S56162
MDCR15 protein - human
C:Species: Homo sapiens (man)
C>Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 08-Oct-1999
C:Accession: S56162
R:Barclay, L.; Loeschner, M.; Tobler, A.; Baggiolini, M.; Moser, B.
Biochem. J. 309, 773-779, 1995

A:Title: Sequence variation of a novel heptahelical leucocyte receptor through alternati
A:Reference number: S56162; MUID:95366951; PMID:763692
A:Accession: S56162
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-327 <BAR>
A:Cross-references: EMBL:X68829; NID:g840783; PIDN:CAA48723.1; PID:g840784
C:Superfamily: vertebrate rhodopsin

Query Match 29.9%; Score 574; DB 2; Length 327;
Best Local Similarity 36.7%; Pred. No. 2e-40;
Matches 122; Conservative 74; Mismatches 118; Indels 18; Gaps 7;

Qy 55 NFKAMPFIMYSIICFVGLNGLVLTYYIFKRLKMTDTYLLNLAVADILFLTPFW 114
Db 3 SFKAFVAVVASLIPFLVIGVNLVILERRQRRSTTEPLFHLAVADLLVFLPFA 62

Qy 115 AVSAKSWFVHFCXLIFAIYKMSFSGMLLLCISIDRYVAIVQAVSAHRHARVLLI 174
Db 63 VAEKSVGWLTGFLCKTVALHKNVFCSSLILACTIADRYAIVAAVHARR--LLS 120

Qy 175 SKLSCVGSAILATVLSIPELLSDQRSSSEQM-RCSLITEH--VEAFITIQVQWVI 230
Db 121 IHTGCTIWLVGFLALPEILPAKYSQGHNNNSLPRCTFSGENQAEHTAMFTSRFLYHA 180

Qy 221 GFLVPLAMSFCYLVITTLQA-RNFRNKAIKVIIVAVVPIVFPOLPYNGVLAQTYA 289
Db 181 GFLPLMLVMGWCVGVVHRLQAQRPRORAKVAVAIIVTSIFFLCWSYHIVIFLDTLA 240

Qy 220 NENIISCTELSKOLNIVDYVYSLACRCCNPFLYAFIVGVKFRNDIFKLFGLGCLSQ 349
Db 241 RIKAVDNTCKLNGSLPVAITMCEPFLGLAHCCINPFLPAGVKERSRLTLKLGCTSP 300

Qy 350 EQLRQ---WSSECRHIRRSMSVEAETTTTS 377
Db 301 ASLQCLFPW-----RRSLSS-ESENATSLT 325

RESULT 9
A53752
Interleukin-8 receptor (clone 5B1a) - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: A53752
R:Prado, G.N.; Thomas, K.M.; Suzuki, H.; Larosa, G.J.; Wilkinson, N.; Folco, E.; Navarro, J.
J. Biol. Chem. 269, 12391-12394, 1994
A:Title: Molecular characterization of a novel rabbit interleukin-8 receptor isoform.
A:Reference number: A53752; MUID:94230294; PMID:8175642
A:Accession: A53752
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-358 <PRA>
A:Cross-references: UNIPROT:P53444; GB:L24445; NID:g437661; PIDN:AAA1378.1; PID:g437662
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 29.9%; Score 574; DB 2; Length 358;
Best Local Similarity 33.8%; Pred. No. 2.2e-40;
Matches 125; Conservative 74; Mismatches 123; Indels 48; Gaps 6;

Qy 30 DDYIDGNTVDY-----TLFESLCSKQDVRFKAMPFIPMYSIICFVGLNGLVLT 83
Db 12 EDFDGFDSNYSYTDLPPLDLSAPCRSESLSTNSVYVLYITLVFLSLGNSLVMVI 71

Qy 84 IYFKRLKMTDTYLLNLAVADILFLTPFMAYSAKSWFVHFCXLIFAIYKMSFSG 143
Db 72 LYSRSTCVTDYLLNLAIADILFAITTPIMAAKRVHGTGTPLCKVSVLYKEVNFYSG 131

Qy 144 MLLLCISIDRYVAIVQAVSAHRHARVLL-----ISKLSVGSAILATVLSIPELL----- 195
Db 132 ILLLCISVDRLAIV-----HATRMIGQRHLYVKFICLSMWGVSLISLPILLFRVA 184

Qy 196 -----YSDLRSSSEQMRCSLITHEVAFTIQAQMTVIGFLVPLAMSFCYLV 245

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Db      185 IRPPNSSPVCEBDMGNSIAKMR-----VLRLLPOTFGILPLMLCYVF 231
Qy      246 IIRTLQANFNENKAIXIYIAVVFVIFQLPQNGVLAQTAVANFITSSTCELSKOLA 305
Db      232 TRLTLQAHMGQHRMRYIFANVLLIFLQMLPYNVLLDTLMRHVIOETERRANDID 291
Qy      306 IAYDTYSIACRCVCNPFVYAFIVKFPNDIKELPKDGLCSQEQOLRQMSCRHIRRS 365
Db      292 RALDAIEILGFLHSCINPIYAFIQQKFRYGLIKLIAHGLISKEFLAKESRSPFVASS 351
Qy      366 MSVEAETTT 375
Db      352 ----GNTSTT 357

RESULT 10
S26667
G:Protein-coupled receptor BLR1 - human
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S26667
R:Dober, T.; Wolf, I.; Emrich, T.; Liipp, M.
Eur. J. Immunol. 22: 2795-2799, 1992
A>Title: Differentiation-specific expression of a novel G protein-coupled receptor from
A:Reference number: S26667; MUID:93049615; PMID:1425907
A:Accession: S26667
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-372 <DOB>
A:Cross-references: UNIPROT:P32302; EMBL:X68149; NID:929459; PIDN:CAA48252.1; PID:929460
C:Genetics:
A:Gene: GDB:BLR1
A:Cross-references: GDB:136235; OMIM:601613
A:Map position: 15q26.1-15q26.1
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match      29.9%; Score 574; DB 2; Length 372;
Best Local Similarity 35.9%; Pred. No. 2,3e-40;
Matches 126; Conservative 78; Mismatches 125; Indels 22; Gaps 9;

Qy      40 DYTLES-LCSKDD--VNRFKAMPIMYSIICFVGLGNGLVLTYYFKRLKMTDT 95
Db      29 DTSLVENHLCPRATEGELMASFKAVFVPVAVSLIFLGVIGNVLVILERRHQRSTST 88
Qy      96 YLLNLAVADILFLTLRPFMAVSAKSMVGVNHCXLIIFAYKMSFSGMILLICISIDRY 155
Db      89 FLPHLAVADLLVFLIRPFAVAGSVGVLTFLCKTVIALHKVNFYCSSLLACIAVDRY 148
Qy      156 VAIVQAVSHRRHARVLLISKSCVSAIATVLSIPELLYSDLORSSSQAM-RCSLLT 214
Db      149 LAIVAVHAYRRR--LISHTICGTYLWVGLLAPLIPILFAYVSGHHNSLPCTPFG 206
Qy      215 EH--VEAFITQAVQMTVIGFLVPLLAISFCYLVIRTLQA-RNFERNKAVIYIAVV 270
Db      207 ENQAEHTAMFTSRFLYHVAAGFLPMLVMGVCYGVVHRLQAQRROQKAVVAILVTS 266
Qy      271 VFIVPOLPQNGVLAQTAVANFITSSTCELSKOLNAYDVYSLACRCVCNPFYAFIG 330
Db      267 IFPLCSPHYIYFLDTLRLAKAVDTCKLNGSLPAIATMCEPLGLAHCCINMLLTFVG 326
Qy      331 VFERNDFIKLFDKGLCSQEQOLRQ-----WSSCHIRRSMSVSEATTTTFS 377
Db      327 VFRSLSLTLTLTGCTGASLCQLRPSW-----RRSLLS-ESENATSLT 370

RESULT 11
JEB0349
interferon-inducible protein 10 (IP-10) receptor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 09-Jul-2004
C:Accession: JEB0349

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R:Tamari, M.; Tomiaga, Y.; Yatsunami, K.; Natumi, S.
Biochem. Biophys. Res. Commun. 251, 41-48, 1998
A>Title: Cloning of the murine interferon-inducible protein 10 (IP-10) receptor and its
A:Reference number: JEB0349; MUID:99009219; PMID:9790904
A:Accession: JEB0349
A:Molecule type: mRNA
A:Residues: 1-367 <TM>
A:Cross-references: UNIPROT:Q9QW06; DDBJ:AB003174; NID:93798731; PIDN:BA34045.1; PID:93;
C:Comment: This protein is important for lymphocyte trafficking to lymphoid organs.
C:Superfamily: vertebrate rhodopsin

Query Match      29.7%; Score 570.5; DB 2; Length 367;
Best Local Similarity 37.0%; Pred. No. 4,3e-40;
Matches 130; Conservative 63; Mismatches 141; Indels 17; Gaps 6;

Qy      32 YIGDNTTYDTLFPES-----LCSKQVRNFKAMFLPIMYSIICFVGLGNGLVLTYY 83
Db      18 FLEENSTPYDGENSDSDSPRCQDPSLNDRFLALYSILFLDLGNGVAAVLY 77
Qy      84 IYFKRLKMTDTYLLNLAVADILFLTLRPFMAVSAKSMVGVNHCXLIIFAYKMSFSEG 143
Db      78 LQRTALSTDTFLHLAVADVLTFLPLMAVDAVQWVFQGLCKVAGALFNINFYAG 137
Qy      144 MLLLCISIDRYVAYIQAASHRRHARVLLISKSCVSAIATVLSIPELLYSDLORSS 203
Db      138 AFLALCISIDRYLSIHAQIYRDRVRV--ALTCIVMGCLLPALDPFYLSDYQ 195
Qy      204 SEQAMRCSLITEVFAFITQAVQMTVIGFLVPLLAISFCYLVIRTLQARNFERNKATK 263
Db      196 RLNATHCQYNPQOV-GRTRYLVQVAGFLPLVMAVYCYAHILANVLVSRGRRRAR 254
Qy      264 VYIAVAVVEIVQLPYNGVLAQTAVANFITSSTCELSKOLNAYDVYSLACRCVCNP 323
Db      255 LVVVVVAAPVAVCMTPFHLVLDLMDVGLARNCGRSHVDVAKSVTSGMGYHCCLP 314
Qy      324 FIYAFIVKFPNDIKELPKDGLCSQEQOLRQMSCRHIRRSMSVSEATTT 373
Db      315 LLYAFVGVKFRQMWMLFRLGRSDQRPQRPSSSR--RESSWS--BT 360

RESULT 12
I38450
chemokine (C-C) receptor 2, splice form A - human
N:Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chem
C:Species: Homo sapiens (man)
C>Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 09-Jul-2004
C:Accession: I38450
R:Chato, I.F.; Myers, S.J.; Herman, A.; Francis, C.; Connolly, A.J.; Coughlin, S.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
A>Title: Molecular cloning and functional expression of two monocyte chemoattractant prot
A:Reference number: A53477; MUID:94195821; PMID:8146186
A:Accession: I38450
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <RES>
A:Cross-references: UNIPROT:P41597; EMBL:U03882; NID:9472555; PIDN:AAA19119.1; PID:94725;
C:Genetics:
A:Gene: GDB:CMKBR2
A:Cross-references: GDB:337364; OMIM:601267
A:Map position: 3p21-3p21
C:Superfamily: vertebrate rhodopsin
C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane
F:44-68/Domain: transmembrane #status predicted <TM1>
F:79-99/Domain: transmembrane #status predicted <TM2>
F:115-136/Domain: transmembrane #status predicted <TM3>
F:154-178/Domain: transmembrane #status predicted <TM4>
F:208-226/Domain: transmembrane #status predicted <TM5>
F:244-265/Domain: transmembrane #status predicted <TM6>
F:292-309/Domain: transmembrane #status predicted <TM7>
F:14-binding site: carbohydrate (Asn) (covalent) #status predicted
F:32-277,113-190/Disulfide bonds: #status predicted

Query Match      29.7%; Score 570; DB 2; Length 374;

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Best Local Similarity 39.6%; Pred. No. 4.9e-40; Matches 128; Conservative 65; Mismatches 110; Indels 20; Gaps 10;

QY 26 DEVTDDYIGDNTTVDYTLTLESLCKSDVNFAMFLPIMYSIICFVGLGNGLVLTYY 85
18 BEVT-----TFPYD-YGAPCHKFDVQIGAQLLPPLYSIVPIFGVGNMLVLLILN 69

QY 86 FRLKLTMTDTYLLNLAADVILFLTLTPFAVSAKSWFGVHFCKLIPAIYKMSFFSGML 145
70 CKKLKCLTDIYLLNLAISDLFLTLPLMAHSAANEMVFGNAMCKLFTGLYHIGVFGGIF 129

QY 146 LILCISIDRYVAIVQAVSAHRRARVLLISKLSGSAIILATVLSIPELYSIDLORSSSE 205
130 FILLITIDRYLAIYVAHVA--LKARTVTFGVVTSVITWLVAVPASVPGIIFPKCKQEDSV 187

QY 206 QAMRCS-LITEHVEAFITIQVQWVIGFLVPLAMSFCLVILIRTLQARN-FERNKAIK 263
188 YV--CGPYPRGMNNFHTIM--RNILGLVLPPLILNIVICSGILKTLRCRNEKKHRAVR 243

QY 264 VLIIVAVVFIIVQLPYNGVLAQTVANFNITSTCELSKOLNIADYVTSIACVRCVNP 323
244 VIFTIMIVFLEWTPYNYIILLNTFOEF-FGLSNCESTSQLDAQVETLGMTHCCINP 302

QY 324 FLVAFIVGKFRNDIFKFLK 346
303 IIVAFVGEKFRS-LFHI--ALGC 322

Db

RESULT 13

JC2443

chemokine (C-C) receptor 2, splice form B - human
N/Alternate names: C-C CR-2; monocyte chemoattractant protein 1 receptor; monocyte chem
C/Species: Homo sapiens (man)
C/Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
C/Accession: J02443; 138463
R/Yamagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.
Biochem. Biophys. Res. Commun. 202, 1156-1162, 1994
A/Title: cDNA cloning and functional expression of a human monocyte chemoattractant prot
A/Reference number: J02443; MUID:94324942; PMID:8048929
A/Accession: J02443
A/Molecule type: mRNA
A/Residues: 1-360 <YAM>
A/Cross-references: UNIPROT:P41597; DDBJ:D29994; NID:g531246; PIDN:BAA06253.1; PID:g5312
R/Charo, I.F.; Myers, S.J.; Herman, A.; Francis, C.; Connolly, A.J.; Coughlin, S.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
A/Title: Molecular cloning and functional expression of two monocyte chemoattractant pro
A/Reference number: A53477; MUID:94195821; PMID:8146186
A/Accession: 138463
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-360 <RES>
A/Cross-references: EMBL:U03905; NID:g472557; PIDN:AAA19120.1; PID:g472558
C/Genetics:
A/Genes: GDB:CMKBR2
A/Cross-references: GDB:337364; OMIM:601267
A/Map position: 3p21-3p21
C/Superfamily: vertebrate rhodopsin
C/Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembran
F/3-10/Domain: transmembrane #status predicted <TM3>
F/81-100/Domain: transmembrane #status predicted <TM2>
F/115-136/Domain: transmembrane #status predicted <TM3>
F/154-178/Domain: transmembrane #status predicted <TM4>
F/207-226/Domain: transmembrane #status predicted <TM5>
F/244-268/Domain: transmembrane #status predicted <TM6>
F/287-309/Domain: transmembrane #status predicted <TM7>
F/14/Binding site: carbohydrate (Asn) (covalent) #status predicted
F/113-190/Disulfide bonds: #status predicted

Query Match 29.5%; Score 567.5; DB 2; Length 360;
Best Local Similarity 39.2%; Pred. No. 7.6e-40;
Matches 125; Conservative 64; Mismatches 113; Indels 17; Gaps 8;

QY 26 DEVTDDYIGDNTTVDYTLTLESLCKSDVNFAMFLPIMYSIICFVGLGNGLVLTYY 85

Db

QY 18 BEVT-----TFPYD-YGAPCHKFDVQIGAQLLPPLYSIVPIFGVGNMLVLLILN 69

QY 86 FRLKLTMTDTYLLNLAADVILFLTLTPFAVSAKSWFGVHFCKLIPAIYKMSFFSGML 145
70 CKKLKCLTDIYLLNLAISDLFLTLPLMAHSAANEMVFGNAMCKLFTGLYHIGVFGGIF 129

QY 146 LILCISIDRYVAIVQAVSAHRRARVLLISKLSGSAIILATVLSIPELYSIDLORSSSE 205
130 FILLITIDRYLAIYVAHVA--LKARTVTFGVVTSVITWLVAVPASVPGIIFPKCKQEDSV 187

QY 206 QAMRCS-LITEHVEAFITIQVQWVIGFLVPLAMSFCLVILIRTLQARN-FERNKAIK 263
188 YV--CGPYPRGMNNFHTIM--RNILGLVLPPLILNIVICSGILKTLRCRNEKKHRAVR 243

QY 264 VLIIVAVVFIIVQLPYNGVLAQTVANFNITSTCELSKOLNIADYVTSIACVRCVNP 323
244 VIFTIMIVFLEWTPYNYIILLNTFOEF-FGLSNCESTSQLDAQVETLGMTHCCINP 302

QY 324 FLVAFIVGKFRNDIFKFLK 342
303 IIVAFVGEKFRYLSVFFR 321

Db

RESULT 14

J01231

interleukin-8 receptor - rabbit
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C/Accession: J01231; A46483
R/Beckmann, M.P.; Mueger, W.E.; Kozlosky, C.; VandenBoe, T.; Price, V.; Lyman, S.; Gerard
Biochem. Biophys. Res. Commun. 179, 784-789, 1991
A/Title: Molecular characterization of the interleukin-8 receptor.
A/Reference number: J01231; MUID:91378994; PMID:1898400
A/Accession: J01231
A/Molecule type: DNA
A/Residues: 1-355 <BEC>
A/Cross-references: UNIPROT:P21109; GB:M74240; NID:g165438; PIDN:AAA1375.1; PID:g165439
R/Lee, J.; Huang, W.J.; Rice, G.C.; Wood, W.T.
J. Immunol. 148, 1261-1264, 1992
A/Title: Characterization of complementary DNA clones encoding the rabbit IL-8 receptor.
A/Reference number: A46483; MUID:92148149; PMID:1737938
A/Accession: A46483
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-355 <LEB>
A/Cross-references: GB:M28273; NID:g165440; PIDN:AAA3176.1; PID:g165441
A/Experimental source: neutrophils
A/Note: sequence extracted from NCBI backbone (NCBI:81526, NCBI:81530)
C/Superfamily: vertebrate rhodopsin
C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match 29.4%; Score 565; DB 2; Length 355;
Best Local Similarity 37.1%; Pred. No. 1.2e-39; Matches 114; Conservative 66; Mismatches 91; Indels 36; Gaps 4;

QY 63 IMYSIICFVGLGNGLVLTYYIFKRLTMTDTYLLNLAADVILFLTLTPFAVSAKSW 122
49 VIALVPLLSILGNSLVWLVLILYSRNSVTDVYLLNLAAMDILPALIMPFAVSKGWM 108

QY 123 VFGVHFCKLIPAIYKMSFFSGMLLILCISIDRYVAIVQAVSAHRRARVLLISKLS 179
109 IFGTPGLCVSVSYKENVFSGILLACISVDYRLAIYVATRTLQKRH-----LVKPIG 162

QY 160 VGSAILATVLSIPEL-----YSDLORSSSEQAMRCSLITEHVEAFITIOV 225
163 LGIMWLSILSLPFLPQVPSPNNSPVCYBDLGHNTAKRM-----VLRI 209

QY 226 AQMVIGFLVPLAMSFCLVILIRTLQARNFERNKAIVLIIVAVVFIIVQLPYNGVLA 285
210 LPHTGFLPPLVLMFCGFTLRLTFOAHMGOKHRAKMRIVRAVVLIFLCCWLPYVLVLA 269

QY 286 QTVANFNITSTCELSKOLNIADYVTSIACVRCVNPFLVAFIVGKFRNDIFKFLK 345

```
Db      270 DILMRTHVIGTQQRNDIDRALDAIEILGFLHSCLNPIIYAFIIGNFRNGFLKMLAARG 329
Qy      346 CLSQEQL 352
Db      330 LRSKEFL 336
```

RESULT 15

S42628

G protein-coupled receptor GPCR6 - mouse

N:Alternate names: interleukin-8 receptor homolog; mubLR1 protein

C:Species: Mus musculus (house mouse)

C:Date: 07-Sep-1994 #sequence_revision 26-May-1995 #text_change 09-Jul-2004

C:Accession: S42628; C48909

R:Kaiser, E.; Foerster, R.; Wolf, I.; Ebensperger, C.; Kuehl, W.M.; Lippe, M.

Eur. J. Immunol. 23, 2532-2539, 1993

A>Title: The G protein-coupled receptor BLR1 is involved in murine B cell differentiation

A:Reference number: S42628; MUID:94009211; PMID:8405054

A:Accession: S42628

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-374 <RA1>

A:Cross-references: UNIPROT:Q04683; EMBL:X71788; NID:92598563; PIDN:CAA50673.1; PID:9433

R:Wilkie, T.M.; Chen, Y.; Gilbert, D.J.; Moore, K.J.; Yu, L.; Simon, M.I.; Copeland, N.G.

Genomics 18, 175-184, 1993

A>Title: Identification, chromosomal location, and genome organization of mammalian G-protein-coupled receptor rhodopsin

A:Reference number: A48909; MUID:94116980; PMID:8288218

A:Accession: C48909

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 151-269 <WIL>

A:Cross-references: GB:L20332; NID:9438798; PIDN:AAA16852.1; PID:9438799

A:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 29.3%; Score 562.5; DB 2; Length 374;
Best Local Similarity 35.2%; Pred. No. 2.1e-39;
Matches 121; Conservative 78; Mismatches 124; Indels 21; Gaps 8;

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Qy      46 SLCSKRD---VRFRKAMFLPIWYSIIICFVGLLGNGLVLTLYIFKRLKMTDLYLNLAV 102
Db      38 NPGSTVEGPLLTSFKAVFMPVAISLIFLLGWMGNILVLTLERHRRHRSSTETFLPHLAV 97
Qy      103 ADILFLLTLPEFMAYSAAKSVFVGFHCKLIFAIYKMSFSGMLLLCISIDRYVAIVQAV 162
Db      98 ADLLLVFLIPFNAVBSGVGVLTGFLCKVYIALHKINFCSSLLVACIADRYLAIVHAV 157
Qy      163 SAHRHRARVLLSKLSCVGSAILATVLSIPELLYSDL-QRSSSEQAMRCSLITEH---VE 218
Db      158 --HAYRRRLLSIHITCTALWLAGFLFALPELLFAKVGQPHNNDLPLQCTFSQENEAEFR 215
Qy      219 APTTIQVAMVIGFLVPLPLAMSCYLIIRTLQA-RNFRNKAIKYIIVVVVPIVFOQL 277
Db      216 AMFTSRFLYHIGFLPMLMGWCYGVVRRLLQAQRPRQAKAVRAIIVTSIFFLCWS 275
Qy      278 PYNGVVLTAQTVAFNITSTCELSKQLINAYDVYSLACVRCVNPFLYFIVGKFRNDI 337
Db      276 PYHIVIFLDTLERLKAVNSCELSGYLSVAITLCEFLGLAHCLINPMLTYFAGVKFRSDL 335
Qy      338 FYLFKDLGCLISQELRQ---WSSCRHRRSSMSVEAETTTFS 377
Db      336 SRLTLKLGCGAPASLCQLFPNW-----RKSSLS-ESNATSLT 372
```

Search completed: February 25, 2005, 02:23:43
Job time : 41 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 25, 2005, 02:06:32 ; Search time 176 Seconds
(without alignments)
1099.806 Million cell updates/sec

Title: US-10-749-990-2

Perfect score: 1922
Sequence: 1 MDLGRPKSVLVALLVIRQ.....RHRRSSMSVEATTTTSP 378

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03 :
1: uniprot_sprot :
2: uniprot_trembl :*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1907	99.2	378	1	CRK7_HUMAN
2	1889	98.3	378	2	Q8H2R6
3	1776	92.4	380	2	O861S1
4	1701	88.5	378	2	O8C8S2
5	1696	88.2	378	1	CRK7_MOUSE
6	1695	88.2	378	2	Q6U2D6
7	1131	58.8	246	2	Q6JXL2
8	1097.5	57.1	358	2	Q6GP68
9	758.5	39.5	357	1	CRK9_HUMAN
10	758.5	39.5	357	1	Q9UQ06
11	748	38.9	359	1	CRK3_MOUSE
12	743.5	38.7	359	2	Q8CH33
13	740.5	38.5	357	2	Q6YT46
14	740.5	38.5	359	2	Q6YT47
15	707.5	36.8	374	1	CRK6_HUMAN
16	703	36.6	367	1	CRK6_MOUSE
17	702	36.5	374	2	Q8H2E7
18	692	36.0	357	2	Q9R1V0
19	681	35.4	358	2	Q42444
20	662	34.4	359	2	Q76LB9
21	655.5	34.1	351	2	Q9E016
22	654.5	34.1	341	2	Q6YT44
23	650.5	33.8	351	2	Q9ERH5
24	648.5	33.7	356	2	Q63ZL5
25	643	33.5	350	1	CRK8_HUMAN
26	629.5	32.8	350	1	Q924I3
27	627.5	32.6	350	2	Q8C0M1
28	626.5	32.6	350	2	Q8O2M9
29	618	32.2	350	1	CRK8_BOVIN
30	614	31.9	360	1	CRK4_HUMAN
31	609	31.7	360	2	Q8MJT8

32	603	31.4	360	2	Q91ZH4	Q91ZH4
33	601.5	31.3	362	2	Q70ZB3	Q70ZB3
34	599.5	31.2	361	2	Q8VHP3	Q8VHP3
35	598.5	31.1	342	1	CRK6_CERAE	Q189D3
36	598.5	31.1	343	1	CRK6_MACMUL	Q9X455
37	597	31.1	342	1	CRK6_MACMUL	Q19024
38	595.5	31.0	342	1	CRK6_MACFA	Q9B466
39	595	31.0	343	1	CRK6_PANTR	Q9TV16
40	595	31.0	360	2	CRK4_MOUSE	P51680
41	591.5	30.8	343	2	Q9N0Z0	Q9N0Z0
42	588.5	30.6	342	1	CRK6_HUMAN	Q00574
43	588.5	30.6	342	2	Q9HCA5	Q9HCA5
44	588	30.6	339	2	Q9TUS4	Q9TUS4
45	585	30.4	339	2	Q9TUS3	Q9TUS3

ALIGNMENTS

RESULT 1
CRK7_HUMAN STANDARD; PRT; 378 AA.
ID CRK7_HUMAN
AC P32248;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE C-C chemokine receptor type 7 precursor (C-C CRK-7) (CC-CRK-7) (CCR-7)
DE (MIP-3 beta receptor) (EBV-induced G protein-coupled receptor 1)
DE (BB1) (BLR2).
GN Name=CRK7; Synonym=CKKBR7, BB1, EV11;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9318173; PubMed=8383238;
RA Birkenbach M.P., Josefsen K., Valamanchi R.R., Lenoir G.M.,
RA Kieff E.;
RT "Epstein-Barr virus-induced genes: first lymphocyte-specific G
RT protein-coupled peptide receptors.";
RL J. Virol. 67:2209-2220(1993).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=95154835; PubMed=7851893;
RA Schweickart V.L., Raport C.J., Godiska R., Byers M.G., Eddy R.L. Jr.,
RA Shows T.B., Gray P.W.;
RT "Cloning of human and mouse BB1, a lymphoid-specific G-protein-
RT coupled receptor encoded on human chromosome 17q12-q21.2.";
RL Genomics 23:643-650(1994).
[3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strassberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schlier G.D.,
RA Altshuler S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toehiyuki S., Carninci P., Prange C.,
RA Raba S.S., Lonnellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richardson S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.T., Skalska U., Smilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Maria W.A.,
RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse CDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: Receptor for the MIP-3-beta chemokine. Probable mediator
CC of EBV effects on B lymphocytes or of normal lymphocyte functions.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in various lymphoid tissues and
CC activated B and T lymphocytes, strongly up-regulated in B cells
CC infected with Epstein-Barr virus and T cells infected with
CC herpesvirus 6 or 7.
CC -1- INDUCTION: By EBV.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
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CC or send an email to license@isb-sib.ch).

CC
DR EMBL, L08176; AAA58615.1; -
DR EMBL, L31584; AAA74230.1; -
DR EMBL, L31582; AAA74230.1; JOINED.
DR EMBL, L31583; AAA74230.1; JOINED.
DR EMBL, L31581; AAA74231.1; -
DR EMBL, BC035343; AAH35343.1; -
DR PIR, A45680; A45680.
DR PIR, B55735; B55735.
DR HSSP, P34996; 1DD0.
DR Genew; HGNC:1608; CCR7.
DR MIM; 600242; -
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0004950; F:chemokine receptor activity; TAS.
DR GO; GO:0004930; F:G-protein coupled receptor activity; TAS.
DR GO; GO:0019735; P:antimicrobial humoral response (sensu Verte. .); TAS.
DR GO; GO:0006935; P:chemotaxis; TAS.
DR GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.
DR GO; GO:0006954; P:inflammatory response; TAS.
DR InterPro; IPR001718; CC_7_receptor.
DR InterPro; IPR000355; Chkline_receptor.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECPT_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECPT_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Signal; Transmembrane.
FT SIGNAL 1 24
FT CHAIN 25 378
FT DOMAIN 25 59
FT TRANSMEM 60 86
FT TRANSMEM 87 95
FT TRANSMEM 96 116
FT DOMAIN 117 130
FT TRANSMEM 131 152
FT DOMAIN 153 170
FT TRANSMEM 171 191
FT TRANSMEM 192 219
FT DOMAIN 220 247
FT TRANSMEM 248 263
FT TRANSMEM 264 289
FT DOMAIN 290 313
FT TRANSMEM 314 331
FT DOMAIN 332 378
FT CARBOHYD 36 36
FT DISULFID 129 210
FT CONFLICT 182 183
FT CONFLICT 337 337
SQ SEQUENCE 378 AA; 42874 MW; D4C84213841A1BD4 CRC64;
Query Match 99.2%; Score 1907; DB 1; Length 378;
Best Local Similarity 99.2%; Pred. No. 7e-106;
Matches 375; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDLGRKMSVSLVVALVYI PQVCLCODEVTDPDYIGDNTVDYTLFESLCSKQDVRNPKAF 60
DB 1 MDLGRKMSVSLVVALVYI PQVCLCODEVTDPDYIGDNTVDYTLFESLCSKQDVRNPKAF 60
QY 61 LPIWTSIICFVGLGNGVLVLYIYIFPKRLKTTDTYTLNLAVADILFLITLFPMAVSAK 120
DB 61 LPIWTSIICFVGLGNGVLVLYIYIFPKRLKTTDTYTLNLAVADILFLITLFPMAVSAK 120
QY 121 SWVFGVHCKLIPAIYKMSFESGMILLICISIDRYVAIVQAVSANRHRARVLLISKLCV 180
DB 121 SWVFGVHCKLIPAIYKMSFESGMILLICISIDRYVAIVQAVSANRHRARVLLISKLCV 180
QY 181 GSALLATVSLIPELLYSDLRSSSQAMRCSLITHEVEAFITIOYAWNIGFVLPLAMS 240
DB 181 GSWLLATVSLIPELLYSDLRSSSQAMRCSLITHEVEAFITIOYAWNIGFVLPLAMS 240
QY 241 FCYLVITLTLQARNFERNKAIKVIAVWVFIVQLPYNQVLAQTVANFNITSSTCEL 300
DB 241 FCYLVITLTLQARNFERNKAIKVIAVWVFIVQLPYNQVLAQTVANFNITSSTCEL 300
QY 301 SKQNLIAVDVYSLACVRCVNPFLYAFIYGVKFRNDIFKLFQDLCLSQEQLRQSSCRH 360
DB 301 SKQNLIAVDVYSLACVRCVNPFLYAFIYGVKFRNDIFKLFQDLCLSQEQLRQSSCRH 360
QY 361 IRRSSMSVEAEFTTTFSP 378
DB 361 IRRSSMSVEAEFTTTFSP 378
RESULT 2
Q8H2R6 PRELIMINARY; PRT; 378 AA.
ID Q8H2R6
AC Q8H2R6;
DT 01-MAR-2003 (TRENBLREL. 23, Created)
DT 01-OCT-2003 (TRENBLREL. 25, Last sequence update)
DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
DE CC chemokine receptor 7.
GN Name=CCR7;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22471764; PubMed=12406887; DOI=10.1182/blood-2002-08-2653;
RA Choi Y.K., Fallert B.A., Murphy-Corb M.A., Reinhardt T.A.;
RT "Simian immunodeficiency virus dramatically alters expression of
RT homeostatic chemokines and dendritic cell markers during infection in
RT vivo.";
RT Blood 101:1684-1691(2003).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL, AF508731; AAN47099.2; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signaln. .; IEA.
DR InterPro; IPR001718; CC_7_receptor.
DR InterPro; IPR000355; Chkline_receptor.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00641; CCEHEMOKINER.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECPT_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECPT_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 378 AA; 42876 MW; D031B848829F08EF CRC64;
Query Match 98.3%; Score 1889; DB 2; Length 378;
Best Local Similarity 98.7%; Pred. No. 8.2e-105;

Matches 373; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDLGKPMKSLVVALVIFQVCLCODEBTDYDYGNTTVDYTLFESLCSKQDVRNFKAW 60
 DB 1 MDLGKPMKSLVVALVIFQVCLCODEBTDYDYGNTTVDYTLFESLCSKQDVRNFKAW 60
 QY 61 LPIWMSIICFVGLGNGLVLTYYIKRLKTMTDYTLNLAVADILFLTLTPMAYSAK 120
 DB 61 LPIWMSIICFVGLGNGLVLTYYIKRLKTMTDYTLNLAVADILFLTLTPMAYSAK 120
 QY 121 SWVFGVHFCCKLFAIYKMSFSGMLLLCISIDRYVAIVQAVSAHRHRAVLLISKLS 180
 DB 121 SWVFGVHFCCKLFAIYKMSFSGMLLLCISIDRYVAIVQAVSAHRHRAVLLISKLS 180
 QY 181 GSAILATVLSIPELYSIDLORSSSEQAMRCSLITHEVAFTITQVAMVIGFVPLIAMS 240
 DB 181 GSAILATVLSIPELYSIDLORSSSEQAMRCSLITHEVAFTITQVAMVIGFVPLIAMS 240
 QY 241 FCYLVIIIRTLQARNFERNKAIKVIIVVVFIVFQLPYNGVLAQTANFNITSTCEL 300
 DB 241 FCYLVIIIRTLQARNFERNKAIKVIIVVVFIVFQLPYNGVLAQTANFNITSTCEL 300
 QY 301 SQQLNINAYDVTYSLACVRCVNPFLYAFIGKFRNDIFKLFKDLGCLSQEQLRWSSCRH 360
 DB 301 SQQLNINAYDVTYSLACVRCVNPFLYAFIGKFRNDIFKLFKDLGCLSQEQLRWSSCRH 360
 QY 361 IRRSSMSVEAETTTTSP 378
 DB 361 IRRSSMSVEAETTTTSP 378

RESULT 3

0861S1 PRELIMINARY; PRT; 380 AA.

AC 0861S1; 01-JUN-2003 (T-EMBLrel. 24, Created)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
 DE Chemokine receptor 7 (Chemokine (C-C motif) receptor 7).
 GN Name=CCR7;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OC NCBI_TaxId=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shinkai H., Muneta Y., Awata T., Uenishi H.,
 RL Submitted (Aug-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Shinkai H., Muneta Y., Eguchi T., Suzuki K., Awata T., Uenishi H.,
 RT "Abstract Molecular cloning and chromosomal assignment to
 SSC12P13->P11 of swine chemokine receptor CCR7.";
 RT Cytogenet. Genome Res. 101:155-160(2003).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Uenishi H., Eguchi T., Suzuki K., Sawazaki T., Toki D., Shinkai H.,
 RA Okumura N., Hamaishi N., Awata T.,
 RT "PDB (Pig EST Data Explorer): construction of a database for ESTs
 derived from porcine full-length cDNA libraries.";
 RT Nucleic Acids Res. 32:D484-D488(2004).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 DR EMBL; AB090872; BAC57929.1; -;
 DR EMBL; AB090870; BAC57929.1; JOINED.
 DR EMBL; AB090871; BAC57929.1; JOINED.
 DR EMBL; AB116555; BAD06309.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.

DR InterPro; IPR001718; CC_7_receptor.
 DR InterPro; IPR000355; Chm_kine_receptor.
 DR InterPro; IPR000276; GPCR_Rhodopn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00657; CCCHMOKINER.
 DR PRINTS; PR00641; CHEMOKINER7.
 DR PRINTS; PR00237; GPCR_RHODOPN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SQ SEQUENCE 380 AA; 42851 MW; 948B2794C6A76AD8 CRC64;

Query Match 92.4%; Score 1776; DB 2; Length 380;
 Best Local Similarity 91.3%; Pred. No. 4.3e-98;
 Matches 347; Conservative 16; Mismatches 15; Indels 2; Gaps 2;

QY 1 MDLGKPM-KSVLVVALVIFQVCLCODEBTDYDYGNTTVDYTLFESLCSKQDVRNFKAW 59
 DB 1 MDLGKPMKSLVVALVIFQVCLCODEBTDYDYGNTTVDYTLFESVCFKQDVRTEFKAW 60
 QY 60 LPIWMSIICFVGLGNGLVLTYYIKRLKTMTDYTLNLAVADILFLTLTPMAYSAK 119
 DB 61 LPIWMSIICFVGLGNGLVLTYYIKRLKTMTDYTLNLAVADILFLTLTPMAYSAK 120
 QY 120 KSWVFGVHFCCKLFAIYKMSFSGMLLLCISIDRYVAIVQAVSAHRHRAVLLISKLS 179
 DB 121 KSWVFGVHFCCKLFAIYKMSFSGMLLLCISIDRYVAIVQAVSAHRHRAVLLISKLS 180
 QY 180 VGSAILATVLSIPELYSIDLORSSSEQAMRCSLITHEVAFTITQVAMVIGFVPLIAMS 239
 DB 181 VGSAILATVLSIPELYSIDLORSSSEQAMRCSLITHEVAFTITQVAMVIGFVPLIAMS 240
 QY 240 SPCLYVIRTLQARNFERNKAIKVIIVVVFIVFQLPYNGVLAQTANFNITST-C 298
 DB 241 SPCLYVIRTLQARNFERNKAIKVIIVVVFIVFQLPYNGVLAQTANFNITSTGTC 300
 QY 299 ELSSQNLINAYDVTYSLACVRCVNPFLYAFIGKFRNDIFKLFKDLGCLSQEQLRWSSC 358
 DB 301 ELSSQNLINAYDVTYSLACVRCVNPFLYAFIGKFRNDIFKLFKDLGCLSQEQLRWSSC 360
 QY 359 RHRRSSMSVEAETTTTSP 378
 DB 361 RHRRSSMSVEAETTTTSP 380

RESULT 4

08CAS2 PRELIMINARY; PRT; 378 AA.

AC 08CAS2; 01-MAR-2003 (T-EMBLrel. 23, Created)
 DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE Mus musculus 16 days neonate thymus cDNA, RIKEN full-length enriched
 DE library, clone:A130067M15 product:chemokine (C-C) receptor 7, full
 DE insert sequence.
 GN Name=Ccr7;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=C57BL/6J; TISSUE=Thymus;
 RC MEDLINE=99279253; PubMed=103496636; DOI=10.1016/S0076-6879(99)03004-9;
 RX Carninci P., Hayashizaki Y.,
 RT "High-efficiency full-length cDNA cloning.";
 RT Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Thymus;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055560;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";

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RL Nature 409:685-690(2001).
RN
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
RN
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kanno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kanno H., Akiyama J., Nishi K., Kikunai T., Taahiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishibe T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda N., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Konda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohnato N., Okazaki Y.,
RA Saito R., Satoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Saeki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tomaru A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AK037965; BAC29909.1; -.
DR WGD; MG1:103011; Ccr7.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0016493; F:C-C chemokine receptor activity; IMP.
DR GO; GO:0006935; P:chemotaxis; IMP.
DR GO; GO:0006955; P:immune response; IMP.
DR InterPro; IPR001718; CC_7_receptor.
DR InterPro; IPR000355; Chemkine_receptor.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR00641; CHEMOKINER7.
DR PRINTS; PR00237; GPCRHHOOPEN.
DR PROSITE; PS00237; G_PROTEIN_RECPT_P1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECPT_P1_2; 1.
DR KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 378 AA; 4285 MW; F027451989B59683 CR64;

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Query Match 88.5%; Score 1701; DB 2; Length 378;
Best Local Similarity 86.2%; Pred. No. 1.2e-93;
Matches 326; Conservative 27; Mismatches 25; Indels 0; Gaps 0;

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QY 1 MDLGRKMSVYVALLVIFQVCLQDEVTDDYIGDNTTVDITLFSLSCKKDVRFKAMF 60

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Db
1 MDLGRKMSVYVALLVIFQVCLQDEVTDDYIGDNTTVDITLFSLSCKKDVRFKAMF 60
QY LPIMYSIIICFVGLGNGVILVITYIFKRLKMTDTYLLNLAVADILFLTLPEMAYSAK 120
Db LPIMYSVLCFVGLGNGVILVITYIFKRLKMTDTYLLNLAVADILFLTLPEMAYSEAK 120
QY 121 SWFGVHFCKLIFAIYKNSPFGMLLLCISIDRVAVVQAVSARHARVLLISKLSGV 180
Db 121 SWFGVYLVCKGIFGIYKNSPFGMLLLCISIDRVAVVQAVSARHARVLLISKLSGV 180
QY 181 GSALATATLSIPELIYSDLPORSSSEQARCSLITEHVEAFITIOVAQWVIGFLVPLAMS 240
Db 181 GIMMLALFLSLPELISGLQKRSGEDTRCSLSVQVBLITIOVAQWVFGFLVPLAMS 240
QY 241 FCYLIIRTLQARNFEENKAIKVIAVVVFVIFQLPYNGVLAQTVANFNITSTCEL 300
Db 241 FCYLIIRTLQARNFEENKAIKVIAVVVFVIFQLPYNGVLAQTVANFNITSTCEL 300
QY 301 SKQLNIADVYSLACVRCQVNPFIYATIGYFRNDIRKLPDGLCLSQEQLRQSSCRH 360
Db 301 SKQLNIADVYSLSASVRCVNPFIYATIGYFRSDIRKLPDGLCLSQEQLRQSSCRH 360
QY 361 IRRSSMSVEARETTTTFSP 378
Db 361 VANNASVSEARETTTTFSP 378

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RESULT 5
CCK7 MOUSE
ID CCK7 MOUSE STANDARD; PRT: 378 AA.
AC P47774;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE C-C chemokine receptor type 7 precursor (C-C-CR-7) (CCR-7)
DE (MIP-3) beta receptor (BBV-induced G protein-coupled receptor 1)
DE (EBI1).
GN Name=Ccr7; Synonyms=Cmbkr7, Ebi1, Ebi1b;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
RX MEDLINE=95154835; PubMed=7851893;
RA Schweickart V.L., Raport C.J., Godiska R., Byers M.G., Eddy R.L. Jr.,
RA Shows T.B., Gray P.W.;
RT "Cloning of human and mouse EBI1, a lymphoid-specific G-protein-
RT coupled receptor encoded on human chromosome 17q12-q21.2.";
RL Genomics 23:643-650(1994).
CC -1- FUNCTION: Receptor for the MIP-3-beta chemokine. Probable mediator
CC of BBV effects on B lymphocytes or of normal lymphocyte functions.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb.ch/announce/
CC or send an email to license@isb.ch).
CC -----
DR EMBL; U31580; AAA74232.1; -.
DR PIR; A55735; A55735.
DR WGD; MG1:103011; Ccr7.
DR GO; GO:0016493; F:C-C chemokine receptor activity; IMP.
DR GO; GO:0006935; P:chemotaxis; IMP.
DR GO; GO:0006955; P:immune response; IMP.
DR InterPro; IPR001718; CC_7_receptor.
DR InterPro; IPR000355; Chemkine_receptor.

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DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G PROTEIN RECEPTOR FL 1; 1.
DR PROSITE: PS00262; G PROTEIN RECEPTOR FL 2; 1.
KM G-protein coupled receptor; Glycoprotein; Signal; Transmembrane.
FT SIGNAL 1 24
FT CHAIN 1 24
FT DOMAIN 25 378
FT TRANSMEM 25 59
FT TRANSMEM 60 86
FT TRANSMEM 87 95
FT TRANSMEM 96 116
FT TRANSMEM 117 130
FT TRANSMEM 131 152
FT TRANSMEM 153 170
FT TRANSMEM 171 191
FT TRANSMEM 192 219
FT TRANSMEM 220 247
FT TRANSMEM 248 263
FT TRANSMEM 264 289
FT TRANSMEM 290 313
FT TRANSMEM 314 331
FT TRANSMEM 332 378
FT CARBOHYD 36 36
FT DISULFID 129 210
SQ SEQUENCE 378 AA; 42941 MW; 42941 MW; ACBIA422CF54A54 CRC64;

Query Match Best Local Similarity 86.0%; Score 1696; DB 1; Length 378;

Matches 325; Conservative 27; Mismatches 26; Indels 0; Gaps 0;

QY 1 MDLGRKMSVLLVALLVIFQVCLCODEVTDDYIGDNTTYDYLFBLSCKQDVNRKAMF 60
DB 1 MDLGRKMSVLLVALLVIFQVCLCODEVTDDYIGDNTTYDYLFBLSCKQDVNRKAMF 60
QY 61 LPIMSIIFGVGLNGVLVLTYYPRKLTMTDTYLLNLAADILFLLTPMAVSAK 120
DB 61 LPIMSIIFGVGLNGVLVLTYYPRKLTMTDTYLLNLAADILFLLTPMAVSAK 120
QY 121 SWFGVHFCKLIPAIYKMSFFSGMLLLCISIDRYVAIVQAVSAHRHRAVLLISLSCV 180
DB 121 SWFGVHFCKLIPAIYKMSFFSGMLLLCISIDRYVAIVQAVSAHRHRAVLLISLSCV 180
QY 121 SWFGVHFCKLIPAIYKMSFFSGMLLLCISIDRYVAIVQAVSAHRHRAVLLISLSCV 180
DB 121 SWFGVHFCKLIPAIYKMSFFSGMLLLCISIDRYVAIVQAVSAHRHRAVLLISLSCV 180
QY 181 GSAILATVLSIPBELYSIDLRSSSEQAMRCSLITHEVEAFITIQVQMYIGFVPLAMS 240
DB 181 GSAILATVLSIPBELYSIDLRSSSEQAMRCSLITHEVEAFITIQVQMYIGFVPLAMS 240
QY 181 GSAILATVLSIPBELYSIDLRSSSEQAMRCSLITHEVEAFITIQVQMYIGFVPLAMS 240
DB 181 GSAILATVLSIPBELYSIDLRSSSEQAMRCSLITHEVEAFITIQVQMYIGFVPLAMS 240
QY 241 FCYLVIRTLQARNFERKAIKVIIVAVVVFIVPOLPYNQVLAQTVANFNITSSCEL 300
DB 241 FCYLVIRTLQARNFERKAIKVIIVAVVVFIVPOLPYNQVLAQTVANFNITSSCEL 300
QY 241 FCYLVIRTLQARNFERKAIKVIIVAVVVFIVPOLPYNQVLAQTVANFNITSSCEL 300
DB 241 FCYLVIRTLQARNFERKAIKVIIVAVVVFIVPOLPYNQVLAQTVANFNITSSCEL 300
QY 301 SKQINAYDVYSLACVRCVNPFLVAFIVGFRNDIFPLFKDLGCLSGEOLRQWSSCRH 360
DB 301 SKQINAYDVYSLACVRCVNPFLVAFIVGFRNDIFPLFKDLGCLSGEOLRQWSSCRH 360
QY 301 SKQINAYDVYSLACVRCVNPFLVAFIVGFRNDIFPLFKDLGCLSGEOLRQWSSCRH 360
DB 301 SKQINAYDVYSLACVRCVNPFLVAFIVGFRNDIFPLFKDLGCLSGEOLRQWSSCRH 360
QY 361 IRRSSMSVEAETTTTSP 378
DB 361 IRRSSMSVEAETTTTSP 378
QY 361 VRNASVSMEAETTTTSP 378
DB 361 VRNASVSMEAETTTTSP 378

RESULT 6

Q6U2D6 PRELIMINARY; PRT; 378 AA.

AC Q6U2D6; PRELIMINARY; PRT; 378 AA.
DT 05-JUL-2004 (TRENBLREL. 27, Created)
DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
DE Chemokine receptor 7-like protein.
GN Name=CCR7;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BN; TISSUE=Lymph node;
RL Quintin G., Voland B., Hoffmeyer A.;
RA Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL: AY379972; AAR24573.1; -
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro: IPR001718; CC 7 receptor.
DR InterPro: IPR000355; Chkline receptor.
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00657; CCHROMOKINER.
DR PRINTS: PR00641; CHEMOKINER.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G PROTEIN RECEPTOR FL 1; 1.
DR PROSITE: PS00262; G PROTEIN RECEPTOR FL 2; 1.
KM G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 378 AA; 42821 MW; A015E711DC4B521F CRC64;

Query Match Best Local Similarity 85.4%; Score 1695; DB 2; Length 378;

Matches 323; Conservative 29; Mismatches 26; Indels 0; Gaps 0;

QY 1 MDLGRKMSVLLVALLVIFQVCLCODEVTDDYIGDNTTYDYLFBLSCKQDVNRKAMF 60
DB 1 MDLGRKMSVLLVALLVIFQVCLCODEVTDDYIGDNTTYDYLFBLSCKQDVNRKAMF 60
QY 61 LPIMSIIFGVGLNGVLVLTYYPRKLTMTDTYLLNLAADILFLLTPMAVSAK 120
DB 61 LPIMSIIFGVGLNGVLVLTYYPRKLTMTDTYLLNLAADILFLLTPMAVSAK 120
QY 121 SWFGVHFCKLIPAIYKMSFFSGMLLLCISIDRYVAIVQAVSAHRHRAVLLISLSCV 180
DB 121 SWFGVHFCKLIPAIYKMSFFSGMLLLCISIDRYVAIVQAVSAHRHRAVLLISLSCV 180
QY 121 SWFGVHFCKLIPAIYKMSFFSGMLLLCISIDRYVAIVQAVSAHRHRAVLLISLSCV 180
DB 121 SWFGVHFCKLIPAIYKMSFFSGMLLLCISIDRYVAIVQAVSAHRHRAVLLISLSCV 180
QY 181 GSAILATVLSIPBELYSIDLRSSSEQAMRCSLITHEVEAFITIQVQMYIGFVPLAMS 240
DB 181 GSAILATVLSIPBELYSIDLRSSSEQAMRCSLITHEVEAFITIQVQMYIGFVPLAMS 240
QY 181 GSAILATVLSIPBELYSIDLRSSSEQAMRCSLITHEVEAFITIQVQMYIGFVPLAMS 240
DB 181 GSAILATVLSIPBELYSIDLRSSSEQAMRCSLITHEVEAFITIQVQMYIGFVPLAMS 240
QY 241 FCYLVIRTLQARNFERKAIKVIIVAVVVFIVPOLPYNQVLAQTVANFNITSSCEL 300
DB 241 FCYLVIRTLQARNFERKAIKVIIVAVVVFIVPOLPYNQVLAQTVANFNITSSCEL 300
QY 241 FCYLVIRTLQARNFERKAIKVIIVAVVVFIVPOLPYNQVLAQTVANFNITSSCEL 300
DB 241 FCYLVIRTLQARNFERKAIKVIIVAVVVFIVPOLPYNQVLAQTVANFNITSSCEL 300
QY 301 SKQINAYDVYSLACVRCVNPFLVAFIVGFRNDIFPLFKDLGCLSGEOLRQWSSCRH 360
DB 301 SKQINAYDVYSLACVRCVNPFLVAFIVGFRNDIFPLFKDLGCLSGEOLRQWSSCRH 360
QY 301 SKQINAYDVYSLACVRCVNPFLVAFIVGFRNDIFPLFKDLGCLSGEOLRQWSSCRH 360
DB 301 SKQINAYDVYSLACVRCVNPFLVAFIVGFRNDIFPLFKDLGCLSGEOLRQWSSCRH 360
QY 361 IRRSSMSVEAETTTTSP 378
DB 361 IRRSSMSVEAETTTTSP 378
QY 361 VRTSVSMEAETTTTSP 378
DB 361 VRTSVSMEAETTTTSP 378

RESULT 7

Q6UJL2 PRELIMINARY; PRT; 246 AA.

AC Q6UJL2; PRELIMINARY; PRT; 246 AA.
DT 05-JUL-2004 (TRENBLREL. 27, Created)
DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
DE Chemokine receptor 7 (Fragment).
GN Name=CCR7;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OX NCBI_Taxid=9913;

[1]

RA SEQUENCE FROM N.A.
 RA Werling D.;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AY277742; AAQ18436.1; ..
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007166; P:G-protein coupled receptor protein signal; ..; IEA.
 DR InterPro; IPR001718; CC_7_receptor.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm 1; 1.
 DR PRINTS; PR00641; CHEMOKINER7.
 DR PRINTS; PR00237; GPCR_RHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 DR KEGG Receptor.
 DR KEGG NON TER
 DR KEGG SEQUENCE 246 AA; 1 1 2621 MW; 3E7BCD127F469608 CRC64;
 DR KEGG FT
 DR KEGG SO

Query Match 58.8%; Score 1131; DB 2; Length 246;
 Best Local Similarity 90.7%; Pred. No. 6.6e-60;
 Matches 224; Conservative 13; Mismatches 8; Indels 2; Gaps 2;

QY 133 FAIYMSFSGMILLCTISIDRYVAIVQAVSHRRARVLLISKSCVGSALIAIVLSIP 192
 DB 1 FAIYMSFSGM-LILCTISIDRYVAIVQAVSHRRARVLLISKSCVGSALIAIVLSIP 59
 QY 193 ELIYSDLRSSSEQMRCSLITTEHVEAFITIQAVQMGFLVPLIAMSFCYLIIRTLQ 252
 DB 60 EVMISGIGKSSSEQLRCSLITTEHVEAFITIQAVQMGVGLIPLIAMSFCYLIIRTLQ 119
 QY 253 ARNERNKAIVIIIAVVVFVIFQIPYNGVLAQTVANFNITST-CELSKQNIADVT 311
 DB 120 ARNERNKAIVIIIAVVVFVIFQIPYNGVLAQTVANFNITSTCELSKQNIADVT 179
 QY 312 YSLACVRCNCPFLYAFIGVPRNDIFLFDIGLGLSGEQLRQWSSCHIRRSSVSAE 371
 DB 180 YSLACVRCNCPFLYAFIGVPRNDIFLFDIGLGLSGEQLRQWSSCHIRRSSVSAE 239
 QY 372 TTTTFSP 378
 DB 240 TTTTFSP 246

RESULT 8
 OGGP68 ID OGGP68 PRELIMINARY; PRT; 358 AA.
 AC OGGP68;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE MGC80638 protein.
 GN Name=MGC80638;
 OS Xenopus laevis (African clawed frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 CC Xenopodina; Xenopus.
 NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marutana K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stappleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ussin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Bork S.S., Loguelfano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

QY	375	TFSP	378
RA	Villation D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Falley J.Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blaesley R.C., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butlerfield Y.S.,		
RA	Krzywinski M.I., Skaleja U., Smallus D.E., Schnerch A., Schein J.E.,		
RA	Jones S.J., Marra M.A.,		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences."		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).		
RL	[2]		
RN	SEQUENCE FROM N.A.		
RP	TISSUE=Spleen;		
RC	Klein S., Gerhard D.S.,		
RA	Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.		
CC	-1 SUBCELLULAR LOCATION: Integral membrane protein (By similarity).		
CC	-1 SIMILARITY: Belongs to family 1 of G-protein coupled receptors.		
DR	EMBL; BC073273; AAM3273.1; -		
DR	GO; GO:0016021; C:Integral to membrane; IEA.		
DR	GO; GO:0014933; F:C-C chemokine receptor activity; IEA.		
DR	GO; GO:0004872; F:receptor activity; IEA.		
DR	GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.		
DR	GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.		
DR	InterPro; IPR001718; CC_7_receptor.		
DR	InterPro; IPR000355; Chklnk_receptor.		
DR	InterPro; IPR00276; GPCR_Rhodopsn.		
DR	Pfam; PF00001; 7tm_1; 1.		
DR	PRINTS; PR00657; CCHMOKINER.		
DR	PRINTS; PR00641; CCHMOKINER7.		
DR	PRINTS; PR00237; GPCR_RHODOPSN.		
DR	PROSITE; PS00237; G_PROTEIN_RECBE_F1_1; 1.		
DR	PROSITE; PS0262; G_PROTEIN_RECBE_F2_1; 1.		
KW	G-protein coupled receptor; Receptor; Transmembrane		
SW	SEQUENCE 358 AA; 40555 MW; D1F3C148823CAD5 CRC64;		
QY	Query Match	57.1%;	Score 1097.5; DB 2; Length 358;
	Best Local Similarity	56.6%;	Pred. No. 8,7e-58;
	Matches 206; Conservative	70;	Mismatches 81; Indels 7; Gaps 3;
QY	16 LVTFQVCLCQDEVDYDIDGNTYDYTLFESLCKKQVRPKMFLPIWYSITCPVGLG	75	
DB	1 MATQLALVGEENVSSTDNVPSITMDYDQIVCCGKGVRRFSFLPAMATYITICLVLAG	60	
QY	76 NGLVVLYIYVYKRLKWTMDYFLNLAAADILFLTLTFPMAYSAKSWVFGVHFKCLTFAI	135	
DB	61 NGLVMIRYLYIYVYKRLKWTMDYFLNLAAADILFLTLTFPMAYSAKSWVFGVHFKCLTFAI	120	
QY	136 YKMSFFSGMILLCLCISIDRYVAIVQAVSAHRHRAVLISKLSCVSGAIIATVLSIBEL	195	
DB	121 YKMSFFSGMILLCLCISIDRYVAIVQAVSAHRHRAVLISKLSCVSGAIIATVLSIBEL	180	
QY	196 YSDLRSSSEQAFNCSLITHEVAEF-ITIQVAQNVIFLVLPLAMSCYLYIIRTLQAR	254	
DB	181 YSGVNNNGG-VNNCIIFFSNISGLSAKLSIQMFPGFPLPLIIMALCYCMIIRKLQAR	238	
QY	255 NFEENKAIKYLIAVAVVFIQQLPYNVGVLAQTVANNTSSNCELSKOLNIADVYSL	314	
DB	239 NFEKRYKAIKYLIAVAVVFIQQLPYNVGVLAQTVANNTSSNCELSKOLNIADVYSL	294	
QY	315 ACVCACVNPFLYAEIGVFRNDIFKLEKDKAGCSQEOELQAROMSCRHIRRSSMSYEAEITTT	374	
DB	295 ACPRCCANFLYALITGKFRNDICLCPKDKAGCSQEOELQAROMSCRHIRRSSMSYEAEITTT	354	

DB 355 TRSP 358

RESULT 9

CCR9_HUMAN STANDARD; PRT; 357 AA.

AC P51686; 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE C-C chemokine receptor type 9 (C-C CKR-9) (CC-CCR-9) (CCR-9) (GPR-9-6).

GN Name=CCR9; Synonyms=CKCR9;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

OX NCBI_TaxID=9606;

RN (1)

RP SEQUENCE FROM N.A.

RA Laurens L., Tiffany H.L., Gao J.-L., Modi W., Murphy P.M., Bonner T.I.; Submitted (Apr-1996) to the EMBL/GenBank/DBJ databases.

RL Submitted (Apr-1996) to the EMBL/GenBank/DBJ databases.

RP SEQUENCE FROM N.A.

RA Warren C.N., Atonstam R.S., Sharma S.V.; "CDNA clones of human proteins involved in signal transduction sequenced by the Guthrie CDNA resource center (www.cdna.org)."; Submitted (Feb-2003) to the EMBL/GenBank/DBJ databases.

RP CHARACTERIZATION.

RX MEDLINE=99248139; PubMed=10229797;

RA Zaballos A., Gutierrez J., Varona R., Ardevin C., Marquez G.; "Identification of the orphan chemokine receptor GPR-9-6 as CCR9, the receptor for the chemokine TECK.";

RL J. Immunol. 162:5671-5675(1999).

RT -1- FUNCTION: Receptor for chemokine SCYA25/TECK. Subsequently transduces a signal by increasing the intracellular calcium ions level. Alternative coreceptor with CD4 for HIV-1 infection.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- TISSUE SPECIFICITY: Highly expressed in the thymus and low in lymph nodes and spleen.

CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.1sb-sib.ch/announce/> or send an email to license@sib-sib.ch).

CC EMBL: U45982; AAA93319.1; --

DR EMBL: AT242127; AA092294.1; --

DR GeneW: HGNC:1610; CCR9.

DR MIM: 604738; --

DR GO: GO:0005887; C: integral to plasma membrane; TAS.

DR GO: GO:0004950; F: chemokine receptor activity; TAS.

DR GO: GO:0006968; P: cellular defense response; TAS.

DR GO: GO:0006935; P: chemotaxis; TAS.

DR GO: GO:0007204; P: cytosolic calcium ion concentration elevation; TAS.

DR GO: GO:0007186; P: G-protein coupled receptor protein signalin. .; TAS.

DR InterPro: IPR004069; CC 9 receptor.

DR InterPro: IPR000355; Chem_kine_receptor.

DR InterPro: IPR000276; GPCR_Rhodopsin.

DR Pfam: PF00001; 7tm_1; 1.

DR PRINTS: PRO1531; CHEMOKINER9.

DR PROSITE: PS00237; GPCR_HODOPSIN.

DR PROSITE: PS00237; G_PROTEIN_RECP_FL_1; 1.

DR PROSITE: PS00237; G_PROTEIN_RECP_FL_2; 1.

KM G-protein coupled receptor; Glycoprotein; Transmembrane.

FT DOMAIN 1 37 Extracellular (Potential).

FT TRANSMEM 38 64 1 (Potential).

PT DOMAIN 65 73 Cytoplasmic (Potential).

FT TRANSMEM 74 94 2 (Potential).

FT DOMAIN 95 108 Extracellular (Potential).

FT TRANSMEM 109 130 3 (Potential).

FT DOMAIN 131 148 Cytoplasmic (Potential).

FT TRANSMEM 149 169 4 (Potential).

FT DOMAIN 170 198 Extracellular (Potential).

FT TRANSMEM 199 226 5 (Potential).

FT DOMAIN 227 242 Cytoplasmic (Potential).

FT TRANSMEM 243 268 6 (Potential).

FT DOMAIN 269 292 Extracellular (Potential).

FT TRANSMEM 293 310 7 (Potential).

FT DOMAIN 311 357 Cytoplasmic (Potential).

FT CARBOHYD 20 20 N-linked (GlcNAc. . .) (Potential).

FT DISULFID 107 186 By similarity.

SO SEQUENCE 357 AA; 40713 MW; 96982B0B922F6631 CRC64;

Query Match 39.5%; Score 758.5; DB 1; Length 357;

Best Local Similarity 42.0%; Pred. No. 1,2e-37;

Matches 150; Conservative 78; Mismatches 106; Indels 23; Gaps 6;

QY 28 VTDDYIGDNT-----VDYLPESLCKKDVNRPKAMPPIWYSICFVGLGNGLVLT 82

DB 1 MADDYSESTSMEDYVNFNFTDFYCEKNNVROFASHFLPPLYLVFVIGALNSLVLY 60

QY 83 YIYFKLKTMTDTYLLNLAVADILFLTLPPNAYSRAKSWFGVHFKLIPIAYKNSFFS 142

DB 61 YWYCRVKMTMDVFLNLAIADLFLVTLPPNAAADQMKFQFMCKVNSWYKNNFYIS 120

QY 143 GMLLLICISIDRYVAIVQVSAHRHARVLLSKSCVSALIAITVLSIPELYSDLQRS 202

DB 121 CVLLIMCISVDRIYAIQAQMARHTWREKRLVSKVCFPIWVAALCIPELIYSQIKER 180

QY 203 SSEQAWRGSLI-----TEHVEAFITIOVAQWIGFVLPLAMSCFVLIYIRTLQARNF 256

DB 181 SG--IAICTWVPSDESTYKLSNLTLYK--ILGFLEPPVNAACCTTIIHTLQKKS 235

QY 257 ERNKAIKVIAVWVFIYFQLPYNGVLAQTVAFNITSSTCELSKOLNIADVTYSLAC 316

DB 236 SKRKALKVITVLTAVLVLSQFPYNCILVQTIIDAVAMPISNCAVSINIDICFQVQTIAF 295

QY 317 VRCCNPFLYAFIYGVKFRNDIFKLPDGLCSQEQRLQWSSCH---IRRSMSVE 369

DB 296 FHSCLNPVLYVFGEFRFDLVKTLNKLGISQ---AQWVSFTRREGSKLSMLDE 349

RESULT 10

ID 09U006 PRELIMINARY; PRT; 369 AA.

AC 09U006; 01-MAY-2000 (T-EMBLrel. 13, Created)

DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)

DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)

DE Chemokine receptor CCR9 (Chemokine (C-C motif) receptor 9, isoform A) (CC chemokine receptor 9A).

GN Name=CCR9;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

OX NCBI_TaxID=9606;

RN (1)

RP SEQUENCE FROM N.A.

RX MEDLINE=99248139; PubMed=10229797;

RA Zaballos A., Gutierrez J., Varona R., Ardevin C., Marquez G.; "Identification of the orphan chemokine receptor GPR-9-6 as CCR9, the receptor for the chemokine TECK.";

RL J. Immunol. 162:5671-5675(1999).

RP SEQUENCE FROM N.A.

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Alechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatcheva L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lonnellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richard S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huijs S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Krzywinski M., Skalska U., Smalls D.E., Scherch A., Schen J.E.,
RA Jones S.J., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[3]
RP SEQUENCE FROM N.A.
RC TISSUE=PCR rescued clones;
RA Director MGC Project;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE FROM N.A.
RA Yu C.-R., Feden K.W.C., Farber J.M.,
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
-1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL: AI133337, CAB43477.1; -;
DR EMBL: BC069678, AA69678.1; -;
DR EMBL: AF145439, AA66699.1; -;
DR GO: GO:0016021; C:Integral to membrane; IEA.
DR GO: GO:0016493; F:C-C chemokine receptor activity; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro: IPR004069; CC_9_receptor.
DR InterPro: IPR000355; Chmkin_receptor.
DR Pfam: PF00001; 7tm 1; 1.
DR PRINTS: PR00657; CCHEMOKINER.
DR PRINTS: PR01531; CCHEMOKINER.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECPT_F1_1; 1.
DR PROSITE: PS00262; G_PROTEIN_RECPT_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SEQUENCE 369 AA; 42015 MW; F27CEA0CFB6844C CRC64;
SQ
Query Match 39.5%; Score 758.5; DB 2; Length 369;
Best Local Similarity 42.0%; Pred. No. 1.3e-37;
Matches 150; Conservative 78; Mismatches 106; Indels 23; Gaps 6;
QY 28 VDDYDIGNDT-----VDYTFESLCSKDVNFKAMFLPIWYITICFVGLNGIVLT 82
DB 13 MADDGSESTSSMEDYVNFNPFYCEKNVQFOPSHFLPIWYITVIGALGNSLVILV 72
QY 83 YIYFKRLKMTDTYLLNLAVADILFLTLFPVAVSAKSWGVHCKLIPAIYKMSFPS 142
DB 73 YVYCCRVKMTMDMFLNLAIADLFLVTLFPVAIAAADMKQTFMCKVKNVMYKNRPS 132
QY 143 GMLLLLCISIDRYVAIVQAVSHRRARVLLSKLSCVGSAITLAVLSIPELLYSDLORS 202
DB 143 CCTLIMCISVDRIYIAIQAMRAHWREKRLYSKWCFTIWLIAALCIPILYISQIKER 192
QY 203 SSEQAMRGSLI-----TEHVAFTIOAVQWVIGFVLLMSFCYLVITITLQARNP 256
DB 193 SG--IATCMVPSDESTYLSKSAVLTKV--ILGFPLVWVACCYTIITHTLQAKKS 247
QY 257 EENKAIKVIAVAVVFIQPLPYNGVVLQGTAVANFITSSTCELSKOLNIAVDYTSIAC 316
DB 248 SSKKALKVITVLTLYFVLVSQFPYNCILVQITIDAYAMFISNCVSNIDICQVOTIAF 307

QY 317 VRCNPNPLVYAPIGVKFRNDIFKLFKDIAGLSQEDLRQWSSCRH-----IRSSMSVE 369
DB 308 FHSCLNPLVYFVGFRFRDVLTKLNKIGCISQ--AAQWSPTRREGSKLUSMLE 361
Result 11
CCR9_MOUSE STANDARD; PRT; 369 AA.
AC CCR9_MOUSE
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE C-C chemokine receptor type 9 (C-C CCR-9) (CC-CCR-9) (CCR-9)
DE (Chemokine C-C receptor 10).
GN Name=CCR9; Synonyms=Cmkbr10;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Thymus;
RA Zaballos A., Gutierrez J., Varona R., Ardavin C., Marquez G.;
RT "Identification of the orphan chemokine receptor GPR-9-6 as CCR9, the
RT receptor for the chemokine TECK.";
J. Immunol. 162:5671-5675(1999).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20069400; PubMed=10602049;
DOI=10.1002/1521-4141(200001)30:1<262::AID-IMMU262>3.0.CO;2-S;
RA Wuerfel M.A., Philippe J.M., Nguyen C., Victorero G., Freeman T.,
RA Wooding P., Mazek A., Mattei M.-G., Møllsen M., Jordan B.R.,
RA Møllsen B., Carrier A., Naquet P.;
RT "The chemokine TECK is expressed by thymic and intestinal epithelial
RT cells and attracts TECK double- and single-positive thymocytes expressing
RT the TECK receptor CCR9.";
Eur. J. Immunol. 30:262-271(2000).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi U., Bono H., Kondo S.,
RA Nikiado I., Oshio N., Saito R., Suzuki H., Yamana H., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schimpl L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Brad D., Brusic V., Chochia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frezer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kongsava A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Nunata K., Okido T., Pavan W.J., Petrea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempke C.A., Setou M., Shmida K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Warande Y., Wells C.,
RA Wilting L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavoian M., Zhu Y., Zimmer A., Carlini P., Hayatsu N.,
RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imocani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
CC -1- FUNCTION: Receptor for chemokine SCYA25/TECK. Subsequently
transduces a signal by increasing the intracellular calcium ions

06YT46
ID 06YT46 PRELIMINARY; PRT; 357 AA.
AC 06YT46;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Chemokine (C-C motif) receptor 9 isoform B.
GN Name=CCR9;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxId=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.,
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AP006184; BAD08644.1; -.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR004069; CC_9_receptor.
DR InterPro; IPR000355; Cmkline_receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01531; CHEMOKINER9.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_REC_P1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_REC_P1_2; 1.
DR G-protein coupled receptor; Receptor; Transmembrane.
KW SEQUENCE 357 AA; 40725 MW; 93F80F90F913337A CRC64;
SQ
Query Match 38.5%; Score 740.5; DB 2; Length 357;
Best Local Similarity 42.5%; Pred. No. 1,4e-36;
Matches 151; Conservative 70; Mismatches 111; Indels 23; Gaps 6;
QY 30 DDYIDNNTV-----DYTLFESLCSKDVNFKAMFLPIMYSIICFVGLAGLVLTYYI 84
DB 3 DDYGDATPSIEDYGNFTTDLFCCKKNHVRQFASHFLPLVWLVIVGAVGSLVILYYW 62
QY 85 YFKRLKMTDTYLLNLAVADILFLTLPPWYSAKSNVGVHFCFLIPAIYKMSFFSGM 144
DB 63 YCTRVKMTDMFLNLAIADILFLVTLPPWMAIADQMKFQFMCKVNVSMYKMFYSCV 122
QY 145 LLLLCISIDRYVAIQAASAHHRARVLLISLSCVGSAILATVLSIPELLYSDIQRSS 204
DB 123 LLIMCISVDRIYALIAQAMRAQTWRQRLYSKLVCEFTVWVMAALCIPELLYS--QVKEE 180
QY 205 EQAMCSLI-----TEHVEAFITIOAQMVGIFLPLAMSFVLYIIRTLLOANRFR 258
DB 161 HDIACITMVPSEDESTNLKSAVLTIKV---ILGFPLPVMVMACTYIIITHILIOAKKSK 237
QY 259 NKAIIVIIAAVVVFIVFQLPYNGVLAQTVANFNITSTCELSKOLNIAYDVYSLACVR 318
DB 228 HKALKVTITLVFLVLSQFPYNCVLLVQTIIDAYTFPISCAVSTNIDICFQVLTQIAFPH 297
QY 319 CCVNPFLYAFGVKRRNDIFKLFDLGLCSQEQOLKQMSCHH---IRSSMSVE 369
DB 238 SCLNPVLVYFGEFRFRDLVTKLNLGCLISQ---AQWVSFTRREGSLKLSMLLB 349

RESULT 14

06YT47
ID 06YT47 PRELIMINARY; PRT; 369 AA.
AC 06YT47;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Chemokine (C-C motif) receptor 9 isoform A (Chemokine C-C motif

DE receptor 9).
GN Name=CCR9;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxId=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.,
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AB119263; BAD12126.1; -.
DR EMBL; AB119263; BAD12126.1; -.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR004069; CC_9_receptor.
DR InterPro; IPR000355; Cmkline_receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01531; CHEMOKINER9.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_REC_P1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_REC_P1_2; 1.
DR G-protein coupled receptor; Receptor; Transmembrane.
KW SEQUENCE 369 AA; 41967 MW; DEBF76538600D620 CRC64;
SQ
Query Match 38.5%; Score 740.5; DB 2; Length 369;
Best Local Similarity 42.5%; Pred. No. 1,5e-36;
Matches 151; Conservative 70; Mismatches 111; Indels 23; Gaps 6;
QY 30 DDYIDNNTV-----DYTLFESLCSKDVNFKAMFLPIMYSIICFVGLAGLVLTYYI 84
DB 15 DDYGDATPSIEDYGNFTTDLFCCKKNHVRQFASHFLPLVWLVIVGAVGSLVILYYW 74
QY 85 YFKRLKMTDTYLLNLAVADILFLTLPPWYSAKSNVGVHFCFLIPAIYKMSFFSGM 144
DB 75 YCTRVKMTDMFLNLAIADILFLVTLPPWMAIADQMKFQFMCKVNVSMYKMFYSCV 134
QY 145 LLLLCISIDRYVAIQAASAHHRARVLLISLSCVGSAILATVLSIPELLYSDIQRSS 204
DB 135 LLIMCISVDRIYALIAQAMRAQTWRQRLYSKLVCEFTVWVMAALCIPELLYS--QVKEE 192
QY 205 EQAMCSLI-----TEHVEAFITIOAQMVGIFLPLAMSFVLYIIRTLLOANRFR 258
DB 193 HDIACITMVPSEDESTNLKSAVLTIKV---ILGFPLPVMVMACTYIIITHILIOAKKSK 249
QY 259 NKAIIVIIAAVVVFIVFQLPYNGVLAQTVANFNITSTCELSKOLNIAYDVYSLACVR 318
DB 250 HKALKVTITLVFLVLSQFPYNCVLLVQTIIDAYTFPISCAVSTNIDICFQVLTQIAFPH 309
QY 319 CCVNPFLYAFGVKRRNDIFKLFDLGLCSQEQOLKQMSCHH---IRSSMSVE 369
DB 310 SCLNPVLVYFGEFRFRDLVTKLNLGCLISQ---AQWVSFTRREGSLKLSMLLB 361

RESULT 15

CCR6_HUMAN
ID CCR6_HUMAN STANDARD; PRT; 374 AA.
AC P51684; P78553; Q92846;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE C-C chemokine receptor type 6 (C-C CCR-6) (CC-CCR-6) (CCR-6) (LARC

DE receptor (GPR-C14) (GPCR4) (Chemokine receptor-like 3) (CCR-L3)
 (DR16).
 GN Name=CCR6; Synonyms=CCR13, CCR6, GPR29, STRL22;
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 CC NCBI_TaxID=9606;
 (1)
 RN SEQUENCE FROM N.A., AND FUNCTION.
 RP MEDLINE=97113465; PubMed=9169459; DOI=10.1074/jbc.272.23.14893;
 RA Baba M., Inai T., Nishimura M., Kakizaki M., Takagi S., Hieshima K.,
 RA Nomiyama H., Yoshie O.;
 RT "Identification of CCR6, the specific receptor for a novel lymphocyte-
 RT directed CC chemokine LARC.";
 RL J. Biol. Chem. 272:14893-14898(1997).
 (2)
 RN SEQUENCE FROM N.A.
 RP Laurens L.V., Modi W., Bonner T.I.;
 RL Submitted (Apr-1996) to the EMBL/GenBank/DBJ databases.
 (3)
 RN SEQUENCE FROM N.A.
 RP MEDLINE=97040707; PubMed=8886020; DOI=10.1006/bpbc.1996.1595;
 RA Zaballo A., Varona R., Gutierrez J., Lind P., Marquez G.;
 RT "Molecular cloning and RNA expression of two new human chemokine
 RT receptor-like genes.";
 RL Biochem. Biophys. Res. Commun. 227:846-853(1996).
 (4)
 RN SEQUENCE FROM N.A.
 RP McCoy R., Perlmuter D.H.;
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 (5)
 RN SEQUENCE FROM N.A.
 RP MEDLINE=97224503; PubMed=9070937; DOI=10.1006/geno.1996.4544;
 RA Liao F., Lee H.-H., Farber J.M.;
 RT "Cloning of STRL22, a new human gene encoding a G-protein-coupled
 RT receptor related to chemokine receptors and located on chromosome
 RT 6q27.";
 RL Genomics 40:175-180(1997).
 (6)
 RN SEQUENCE FROM N.A.
 RP Warren C.N., Aronstam R.S., Sharma S.V.;
 RT "cDNA clones of human proteins involved in signal transduction
 RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 (7)
 RN SEQUENCE FROM N.A.
 RP MEDLINE=22935763; PubMed=14574404; DOI=10.1038/nature02055;
 RA Mungall A.J., Palmer S.A., Sims S.K., Edwards C.A., Ashurst J.L.,
 RA Winkling L., Jones M.C., Horton R., Hunt S.E., Scott C.E.,
 RA Gilbert J.G.R., Clamp M.E., Bethel G., Milne S., Alincough R.,
 RA Almeida J.P., Ambrose K.D., Andrews T.D., Ashwell R.I.S.,
 RA Babbage A.K., Bagguley C.L., Bailey J., Banerjee R., Barker D.J.,
 RA Barlow K.F., Bates K., Beare D.M., Beasley H., Beasley O., Bird C.P.,
 RA Blakey S.E., Bray-Allen S., Brock J., Brown A.J., Brown J.Y.,
 RA Burford D.C., Burrill W., Burton J., Carter C., Carter N.P.,
 RA Chapman J.C., Clark S.Y., Clark G., Clee C.M., Clegg S., Cobley V.,
 RA Collier R.E., Collins J.B., Colman L.R., Corby R.N., Coville G.J.,
 RA Culley K.M., Dhali P., Davies J., Dunn M., Earthworm M.E.,
 RA Ellington A.E., Evans K.A., Faulkner L., Francis M.D., Frankish A.,
 RA Frankland J., French L., Garner P., Garnett U., Ghori M.J.,
 RA Gilly L.M., Gillson C.J., Gilchrist R.J., Graham D.V., Grant M.,
 RA Griddle S., Griffiths C., Griffiths M.N.D., Hall R., Hall K.S.,
 RA Hammond S., Harley J.L., Hart E.A., Heath P.D., Heathcote R.,
 RA Holmes S.J., Howden P.J., Howe K.L., Howell G.R., Huckle E.,
 RA Humphrey S.J., Humphries M.D., Hunt A.R., Johnson C.M., Joy A.A.,
 RA Kay M., Keenan S.J., Kimberley A.M., King A., Laird G.K., Langford C.,
 RA Lawlor S., Leongamornlert D.A., Leverhulme M., Lloyd C.R., Lloyd D.M.,
 RA Loveland J.E., Lovell J., Martin S., Mashreghi-Mohammadi M.,
 RA Maassen G.L., Mathews L., McCann O.T., McLaren S.J., McLeay K.,
 RA McMurray A., Moore M.J.F., Mullikin J.C., Niblett D., Nickerson T.,
 RA Novik K.L., Oliver K., Overton-Larty E.K., Parker A., Patel R.,
 RA Pearce A.V., Peck A.I., Phillimore B.J.C.T., Phillips S., Plumb R.W.,
 RA Porter K.M., Ramsey Y., Randy S.A., Rice C.M., Ross M.T., Seale S.M.,

RA Sehna H.K., Sheridan E., Skuce C.D., Smith S., Smith M., Spraggon L.,
 RA Squares S.L., Steward C.A., Sycamore N., Tamlyn-Hall G., Teeter J.,
 RA Theaker A.J., Thomas D.W., Thorpe A., Tracey A., Tromans A., Tubby B.,
 RA Wall M., Wallis J.M., West A.P., White S.S., Whitehead S.L.,
 RA Whitaker H., Wild A., Willey D.J., Wilmer T.E., Wood J.M., Wray P.W.,
 RA Wyatt J.C., Young L., Younger R.M., Bentley D.R., Coulson A.,
 RA Durbin R., Hubbard T., Suleston J.E., Dunham I., Rogers J., Beck S.;
 RT "The DNA sequence and analysis of human chromosome 6.";
 RL Nature 425:805-811(2003).
 (8)
 RN SEQUENCE FROM N.A.
 RP TISSUE=Pancreas;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheef C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Umed T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.V., Lu X., Gibbs R.A.,
 RA Fahy J., Helton B., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.T., Skalska U., Smalls D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 (9)
 RN SEQUENCE FROM N.A.
 RP MEDLINE=97224503; PubMed=9070937; DOI=10.1006/geno.1996.4544;
 RA Liao F., Lee H.-H., Farber J.M.;
 RT "Cloning of STRL22, a new human gene encoding a G-protein-coupled
 RT receptor related to chemokine receptors and located on chromosome
 RT 6q27.";
 RL Genomics 40:175-180(1997).
 (10)
 RN SEQUENCE FROM N.A.
 RP MEDLINE=97224503; PubMed=9070937; DOI=10.1006/geno.1996.4544;
 RA Liao F., Lee H.-H., Farber J.M.;
 RT "Cloning of STRL22, a new human gene encoding a G-protein-coupled
 RT receptor related to chemokine receptors and located on chromosome
 RT 6q27.";
 RL Genomics 40:175-180(1997).
 (11)
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 RP MEDLINE=97224503; PubMed=9070937; DOI=10.1006/geno.1996.4544;
 RA Liao F., Lee H.-H., Farber J.M.;
 RT "Cloning of STRL22, a new human gene encoding a G-protein-coupled
 RT receptor related to chemokine receptors and located on chromosome
 RT 6q27.";
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 (27)
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 RA Liao F., Lee H.-H., Farber J.M.;
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 (28)
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 RP MEDLINE=97224503; PubMed=9070937; DOI=10.1006/geno.1996.4544;
 RA Liao F., Lee H.-H., Farber J.M.;
 RT "Cloning of STRL22, a new human gene encoding a G-protein-coupled
 RT receptor related to chemokine receptors and located on chromosome
 RT 6q27.";
 RL Genomics 40:175-180(1997).
 (29)
 RN SEQUENCE FROM N.A.
 RP MEDLINE=97224503; PubMed=9070937; DOI=10.1006/geno.1996.4544;
 RA Liao F., Lee H.-H., Farber J.M.;
 RT "Cloning of STRL22, a new human gene encoding a G-protein-coupled
 RT receptor related to chemokine receptors and located on chromosome
 RT 6q27.";
 RL Genomics 40:175-180(1997).
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 RA Liao F., Lee H.-H., Farber J.M.;
 RT "Cloning of STRL22, a new human gene encoding a G-protein-coupled
 RT receptor related to chemokine receptors and located on chromosome
 RT 6q27.";
 RL Genomics 40:175-180(1997).
 (31)
 RN SEQUENCE FROM N.A.
 RP MEDLINE=97224503; PubMed=9070937; DOI=10.1006/geno.1996.4544;
 RA Liao F., Lee H.-H., Farber J.M.;
 RT "Cloning of STRL22, a new human gene encoding a G-protein-coupled
 RT receptor related to chemokine receptors and located on chromosome
 RT 6q27.";
 RL Genomics 40:175-180(1997).
 (32)
 RN SEQUENCE FROM N.A.
 RP MEDLINE=97224503; PubMed=9070937; DOI=10.1006/geno.1996.4544;
 RA Liao F., Lee H.-H., Farber J.M.;
 RT "Cloning of STRL22, a new human gene encoding a G-protein-coupled
 RT receptor related to chemokine receptors and located on chromosome
 RT 6q27.";
 RL Genomics 40:175-180(1997).
 (33)
 RN SEQUENCE FROM N.A.
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 RA Liao F., Lee H.-H., Farber J.M.;
 RT "Cloning of STRL22, a new human gene encoding a G-protein-coupled
 RT receptor related to chemokine receptors and located on chromosome
 RT 6q27.";
 RL Genomics 40:175-180(1997).
 (34)
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 RA Liao F., Lee H.-H., Farber J.M.;
 RT "Cloning of STRL22, a new human gene encoding a G-protein-coupled
 RT receptor related to chemokine receptors and located on chromosome
 RT 6q27.";
 RL Genomics 40:175-180(1997).
 (35)
 RN SEQUENCE FROM N.A.
 RP MEDLINE=97224503; PubMed=9070937; DOI=10.1006/geno.1996.4544;
 RA Liao F., Lee H.-H., Farber J.M.;
 RT "Cloning of STRL22, a new human gene encoding a G-protein-coupled
 RT receptor related to chemokine receptors and located on chromosome
 RT 6q27.";
 RL Genomics 40:175-180(1997).
 (36)
 RN SEQUENCE FROM N.A.
 RP MEDLINE=97224503; PubMed=9070937; DOI=10.1006/geno.1996.4544;
 RA Liao F., Lee H.-H., Farber J.M.;
 RT "Cloning of STRL22, a new human gene encoding a G-protein-coupled
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 (37)
 RN SEQUENCE FROM N.A.
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DR InterPro; IPR004067; CC 6 receptor.
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DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR01529; CHEMOKINER6.
DR PRINTS; PR00237; GPCR_RHODOPSN.
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DR PROSITE; PS00262; G_PROTEIN_REC_P1_2; 1.
DR PROSITE; PS00262; G_PROTEIN_REC_P1_3; 1.
DR G-protein coupled receptor; Glycoprotein; Transmembrane.
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QY 202 SSSSEQAMNC---SLITEHVEAFITIQVAMVIGFLVPLIAMSFCYLVIRITLQARNF 257
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